



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 164571

TO: Bao-Qun Li
Art Unit: 1648
Location: rem/3D24/3C18
Serial Number: 09/718803

Wednesday, April 12, 2006

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>.

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).



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78206
STIC-Biotech/ChemLib

184571 ME

From: Li, Bao-Qun
Sent: Friday, April 07, 2006 7:50 AM
To: STIC-Biotech/ChemLib
Subject: 09,718,803

Please do the sequence homology and interference search for SEQ.ID NO: 2 and 5. Thanks.

Bao Qun Li M.D
TC 1600
Art Unit 1648
Tel. 517-272-0904
REM, 3C18
Rm. 3D24

2aa 117
5aa 366

ME

Earlier date: 1999, 11-22

Paul, Shappner
Stephen Jaspers

Theresa Delsham
Paul D Bishop

1 check call adp
patent
102 engine
interference reject

4/12
FBA

3

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

✓ Other CGN

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:29:03 ; Search time 37.8882 Seconds
(without alignments) 929.454 Million cell updates/sec

Title: US-09-718-803A-5
Perfect score: 1905
Sequence: 1 MWNPSPSEPGFNLTLADLD.....KLSTLKDESSRAWTESSINT 366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database :      PIR_80:*
1:  _pir1:
2:  _pir2:
3:  _pir3:
4:  _pir4:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	461.5	24.2	424	2	JH0164	neurotensin recept
2	461.5	24.2	477	2	JC7913	capa receptor (CG1
3	460	24.1	418	2	S29506	neurotensin recept
4	440	23.1	595	2	JC8012	G protein-coupled
5	434.5	22.8	658	2	JC8011	G protein-coupled
6	413	21.7	418	2	A88013	protein K10B4.4 [i
7	405	21.3	416	2	S68822	neurotensin recept
8	390.5	20.5	380	2	S3143	kappa opioid recep
9	383.5	20.1	380	2	A48227	kappa opioid recep
10	379.5	19.9	380	2	JC3434	kappa opioid recep
11	375.5	19.7	380	2	A55259	kappa opioid recep
12	372.5	19.6	380	2	JC2338	kappa opioid recep
13	365.5	19.2	373	2	JE0087	delta opioid recep
14	359	18.8	367	2	JC3421	opioid receptor ho
15	359	18.8	367	2	I49022	kappa opioid recep
16	359	18.8	367	2	I56520	G protein-coupled
17	358.5	18.8	370	2	S43087	orphan opioid rece
18	357.5	18.8	392	2	S65693	opioid receptor mu
19	356	18.7	372	2	S34592	delta opioid recep
20	355	18.6	372	2	B48227	delta opioid recep
21	355	18.6	378	2	I15816	hypothetical prote
22	353.5	18.6	398	2	I56517	mu opioid receptor
23	352.5	18.5	400	2	I56553	mu opiate receptor
24	351.5	18.5	398	2	A57510	mu opioid receptor
25	351.5	18.5	398	2	I56504	mu opioid receptor
26	349	18.3	352	2	JE0296	thyrotropin releas
27	349	18.3	384	2	A47249	brain-specific som
28	347.5	18.2	372	2	I38532	delta opioid recep
29	343	18.0	384	2	JC4629	somatostatin recep

ALIGNMENTS

RESULT 1

neurotensin receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: JH0164
 R:Tanaka, K.; Masu, M.; Nakanishi, S.
 Neuron 4, 847-854, 1990
 A:Title: Structure and functional expression of the cloned rat neurotensin receptor.
 A:Reference number: JH0164; MUID:90297956; PMID:1694443
 A:Accession: JH0164
 A:Molecule type: mRNA
 A:Residues: 1-424 <TM>
 A:Cross-references: UNIPROT:P20789; UNIPARC:UPI00001305AF
 C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor.
 cter (neuromodulator in the brain and as a hormone) cellular mediator in peripheral
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
 F:65-87/Domain: transmembrane #status predicted <TM1>
 F:97-121/Domain: transmembrane #status predicted <TM2>
 F:144-165/Domain: transmembrane #status predicted <TM3>
 F:189-210/Domain: transmembrane #status predicted <TM4>
 F:236-260/Domain: transmembrane #status predicted <TM5>
 F:309-330/Domain: transmembrane #status predicted <TM6>
 F:348-372/Domain: transmembrane #status predicted <TM7>
 F:438-472/Binding site: carboxylate (Asn)(covalent) #status predicted

Query Match	24.2%	Score	461.5	DB 2	Length	424			
Best Local Similarity	33.5%	Pred. No.	1.5e-32						
Matches	120	Conservative	67	Mismatches	120	Indels	51	Gaps	12

Qy	3	NATPSEEPGENLTADLDWDASPCNDLSGDELLQLFPAPILLAGVTATCTALFPVVGIAGNL	62
Db	42	NTSESOTAGPN---SDLD-----VNTDIYSKVL-----VTALYLALFPVVGTVGNS	83
Qy	63	LTMVLVSR----FRELRTTNLYLSSMAFSDLLI--FLCWLPLDLVR-LWQYRWNFGDL LCK	117
Db	84	VTAFTLARKKSLSQSTVYHGLGSLASDLLILLAMPVELYNFIWVHHFWAEGDAGR	143
Qy	118	LFOVSESCTATVLTITLALSVERYFAICPPLRAKVVTVKGRVKLVFIWVAVAFCSAGP	177
Db	144	GYFLRDACTATALNVASLSVERYLAIChPFKAKTLMRSRTKFFISAIWLASALLAIP	203
Qy	178	IFVLVGVEHE--NGTDPWDNTNECRPTPEAVRSGLLTVMVWVSSLPFEL-PVFCITLVLSL	234
Db	204	MLFTMTGLQNRSGDGHFGGL-VCTP---IVDTATVKVVIQVNTFMSFLFPMPLVSI LNTV	259
Qy	235	IGKILMRRRRGDADVVGASL-----RDONHKQTVKMLAVVVVFAPIL	274
Db	260	IANKLTVMVHQAAEQGRVCTVGTHTNGLEHSTFNNTIEPGRVQALRHGVLVLRVAVI FVV	319
Qy	275	CWLFPFHVGRYLF8K-SPEPGSLEIAQISOYCNLSVFLVLSAAINPILYNIMSKKYR	331

A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes
 A:Reference number: A75000; PMID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/Celegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: A88013

Db	7	WPPRPSAGLSL-----EARLGVDT-----RLWAKVLF-----TALYSLIFAFGTAGN	50
Qy	62	LLTLMVVSRFRRELRT-TTNLYLSSMAFSDLLIEFL-CMPDLVLVR-LWQYPWNFGDLLCKL	118

QY 62 LITMLVYSRFRLEIRT-TTNLYLSSMAFSDLLIFL-CMPDLVLR-LWQYRPWNFGDLLCKL 118

QY 134 ITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIMAVAFCSAGPIFVLVGVHEHNGT--- 190
Db 149 LTMSVDVRYIAVCHPVKALDFTPLKAKIINICIMLLA--SSVGISAIVLG-----GTVKR 202
QY 191 DPWDTNECR---PTEFAVRSGLLTVMVWVSSIRFEFLPVFCITLVLYSLIGRKLWRRRGD 246
Db 203 EDVDVIECSLQPPDDEYSWDLFMKICVFVFA--FVIVPLIIVCYITLM---ILRLKSVR 257
QY 247 AVVGASLRDONHKTQVKMLAVVVFAPILCWLPFFHVGRLYLFSGSPFSGLEIAQISQYCNL 306
Db 258 LLGSGREKDRNLRRITKLVLVAVVAFIICWTPHI--FILVEALGSTSHSTAALSSYYFC 315
QY 307 VSVFLFYLSAAINPILYNIMSKYRVAVFRLIGF-----EPFSQRLKSLTKDESS 356
Db 316 IA--LGYTNSSLNPVLYAFLDENFK-RCFRDPCFPPIKMRERQSTNRVNTVQDPAS 369

RESULT 10
JC2434
kappa opioid receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: JC2434
R:Nishi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.
Biochem. Biophys. Res. Commun. 205, 1353-1357, 1994
A:Title: Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor
A:Reference number: JC2434; MUID:95100967; PMID:7802669
A:Accession: JC2434
A:Molecule type: mRNA
A:Residues: 1-380 <NIS>
A:Cross-references: UNIPROT:P33534; UNIPARC:UPI000016CF1C; DDBJ:D31663
C:Genetics:
A:Map position: 1A2-3
A:Introns: 86/2; 204/1
C:Superfamily: vertebrate rhodopsin
C:Keywords: receptor

Query Match 19.9%; Score 379.5; DB 2; Length 380;
Best Local Similarity 26.9%; Pred. No. 1.8e-25;
Matches 98; Conservative 76; Mismatches 137; Indels 53; Gaps 10;

QY 20 DWDASPGNDSLQDELQLFPA-----PLLAGVTATCVAFVVGIAGNLLTMLVVSRRPRE 73
Db 32 NWAESDSNGSYGSEDQQLSAHISPAIPVI--ITAVSVFVVGVLGNSLVMFVIIRYTK 89
QY 74 LRTTNLYLSSMAFSDLLIFLCMPLDLVRLMQYRPWFNFGDLLCKLFQVSSSCTYATVLT 133
Db 90 MKTATNIYIFNLADALVTTTTPQSA-VYLMSWPFPGDVLCKIVISIDYNNMFTSIFT 148
QY 134 ITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIMAVAFCSAGPIFVLVGVHEHNGTDP- 192
Db 149 LTMSVDVRYIAVCHPVKALDFTPLKAKIINICIMLLA--SSVGISAIVLGTVKVEDVDVI 208
QY 193 -----WDTECRTEFAVRSGLLTVMVWVSSIRFFLPVFCITLVLYSLIGRKL 239
Db 209 ECLLQFPDDDEYSWD-----LFMKICVVVFAFVPLIIVCYITLM---I 250
QY 240 WRRRGDAVVGASLRDONHKTQVKMLAVVVFAPILCWLPFFHVGRLYLFSGSPFSGLEIAQ 299
Db 251 LRLKSVRLSGREKDRNLRRITKLVLVAVVAFIICWTPHI--FILVEALGSTSHSTA 308
QY 300 ISOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLIGF-----EPFSQRLKSLTK 352
Db 309 LSSYYFCIA--LGYTNSSLNPVLYAFLDENFK-RCFRDPCFPPIKMRERQSTNRVNTVQ 365
QY 353 DESS 356
Db 366 DPAS 369

RESULT 11

A55259

kappa opioid receptor - guinea pig

N:Alternate names: dynorphin receptor
C:Species: Cavia porcellus (guinea pig)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55259
R:Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A.; Wats.
Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994
A:Title: Primary structure and functional expression of a guinea pig kappa opioid (dyn.
A:Reference number: A55259; MUID:94224825; PMID:8170987
A:Accession: A55259
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-380 <XIE>
A:Cross-references: UNIPROT:P41144; UNIPARC:UPI0000130D98; GB:U04092; NID:G476106; PID:
C:Superfamily: vertebrate rhodopsin
C:Keywords: transmembrane protein

Query Match 19.7%; Score 375.5; DB 2; Length 380;
Best Local Similarity 28.4%; Pred. No. 4.1e-25;
Matches 92; Conservative 79; Mismatches 122; Indels 31; Gaps 11;

QY 21 WDASPGNDSLQDELQLFPA-----PLLAGVTATCVAFVVGIAGNLLTMLVVSRRPREL 74
Db 33 WAEPDGNAGSAGPQDELEPAHISPAIPVI--ITAVSVFVVGVLGNSLVMFVIIRYTKM 90
QY 75 RTTNLYLSSMAFSDLLIFLCMPLDLVRLMQYRPWFNFGDLLCKLFQVSSSCTYATVLT 134
Db 91 KTATNIYIFNLADALVTTTTPQST-VYLMSWPFPGDVLCKIVISIDYNNMFTSIFTL 149
QY 135 TALSVERYFAICFPLRAKVVVTKGRVKLVIFVIMAVAFCSAGPIFVLVGVHEHNGT---D 191
Db 150 TMSVDVRYIAVCHPVKALDFTPLKAKIINICIMLLA--SSVGISAIVLG-----GTVKRE 203
QY 192 PWDTECR---PTEFAVRSGLLTVMVWVSSIRFFLPVFCITLVLYSLIGRKLWRRRGDA 247
Db 204 DVDIECSLQFPDDDDYSWDLFMKICVFVFA--FVIVPLIIVCYITLM---ILRLKSVRL 258
QY 248 VVGASLRDONHKTQVKMLAVVVFAPILCWLPFFHVGRLYLFSGSPFSGLEIAQISOYCNLV 307
Db 259 LSGSREKDRNLRRITKLVLVAVVAFIICWTPHI--FILVEALGSTSHSTAALSSYYFCI 316
QY 308 SFVLFYLSAAINPILYNIMSKYR 331
Db 317 A--LGYTNSSLNPVLYAFLDENFK 338

RESULT 12

JC2338

kappa opioid receptor 1 - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: JC2338; A55354; I57005; G01546

R:Manson, E.; Bare, L.; Yang, D.

Biochem. Biophys. Res. Commun. 202, 1431-1437, 1994

A:Title: Isolation of a human kappa opioid receptor cDNA from placenta.

A:Reference number: JC2338; MUID:94338360; PMID:8060324

A:Accession: JC2338

A:Molecule type: mRNA

A:Residues: 1-380 <MAN>

A:Cross-references: UNIPROT:P41145; UNIPARC:UPI0000001257; GB:U11053; NID:G532059; PIDN:

A:Experimental source: placenta

R:Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.

J. Biol. Chem. 269, 25966-25969, 1994

A:Title: Human kappa opiate receptor second extracellular loop elevates dynorphin's aff

A:Reference number: A55354; MUID:95014415; PMID:7929306

A:Accession: A55354

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 136-279 <WAN>

A:Cross-references: UNIPARC:UPI000016ABBA; GB:L36130; NID:G598184; PIDN:AAA63646.1; PID:

R:Zhu, J.; Chen, C.; Xue, J.

Life Sci. 56, 201-207, 1995

A:Title: Cloning of a human kappa opioid receptor from the brain.

A:Reference number: I57005

Query Match	18.8%;	Score 359;	DB 2;	Length 367;
Best Local Similarity	29.5%;	Pred. No. 1.1e-23;		
Matches	98;	Conservative	70;	Mismatches 120;
			Indels	44;
			Gaps	12;

QY	26	GNDSGLDELQLQLPAPLL-----AGVTATCVALFVV-----GIAGNLLTMLVVSRRF	71
DB	20	GNLSLNETV---PHLLLNASHAFPLGPKVTIVGLYLAVCIGGLGCLVMYVILRH	76
QY	72	RELRTTNLYSSMAFSDLLIFLCMPL-----DLVRLWQYRPWFNFGLLCKLFQFVSBSECTY	128
DB	77	TKMKTATNIYFNALADTLVLLTLPQGTDILLGF----WPFGNALCKTVIALDYYNMF	132
QY	129	ATVLTITALLSVERYFAICPLPRAKVVTKGRVKLVFIWIAVAFCSAGPIFVLVGEHEN	188
DB	133	TSTFTLTAMSDVRYVAICHPIRALDVRTSSKAQAVNVAIWALASVVGVPVAIMGSAQVED	192
QY	189	GTDPMWDTNECR---PTIEFAYRSGLLITVMWVSSIFPELPVFCLTIVLYSLIGRKLWRRRRG	245
DB	193	-----BEIECLVIPAQDWGVPVFAICIFLS--FIIPVLLIISVCYSLMIRRL-----RG	241
QY	246	DAVV--GASLRDQNHKOTVKMLAVVVFPAFICLWLPFHVGRVLYFSKSPSGLEIAQISOYC	304
DB	242	VRLLSSGRKDRMLRRIITRLVIVVAVFVGCWTFVQVFLVQGLGVQPGSETAVAILRFC	301
QY	305	NLVSVFLFYLSAAINPILYNIMSKYRVAVFR	336
DB	302	T-----ALGYVNSCLNPILYAFLDENFK--ACFR	328

Search completed: April 10, 2006, 17:34:31
Job time : 38.8882 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:23:48 ; Search time 65.646 Seconds
(without alignments)
783.099 Million cell updates/sec

Title: US-09-718-803A-2

Perfect score: 611

Sequence: 1 MPSPTGTCVSLLLGLMLDL.....LGKFLQDILMEAKEAPADK 117

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	100.0	117	2	AAW87991 Protein d
2	611	100.0	117	3	AAW87236 Human sig
3	611	100.0	117	4	AAW20101 Zsig33 pr
4	611	100.0	117	4	AAW62649 Human zsi
5	611	100.0	117	4	AAW38890 Human pol
6	611	100.0	117	4	AAW60511 Human ghr
7	611	100.0	117	5	AAW78319 Amino aci
8	611	100.0	117	5	AAW23838 Human zsi
9	611	100.0	117	5	AAW15883 Human zsi
10	611	100.0	117	6	AAW58046 Human PRO
11	611	100.0	117	6	AAW59124 Novel hum
12	611	100.0	117	6	AAW82636 Human sec
13	611	100.0	117	6	AAW17836 Novel hum
14	611	100.0	117	6	AAW60555 Human sec
15	611	100.0	117	6	AAW13937 Human PRO
16	611	100.0	117	6	AAW81090 Human PRO
17	611	100.0	117	6	AAW72522 Novel hum
18	611	100.0	117	6	AAW66790 Human PRO
19	611	100.0	117	6	AAW59871 Novel sec
20	611	100.0	117	6	AAW59271 Human sec
21	611	100.0	117	6	AAW25968 Human PRO
22	611	100.0	117	6	AAW25061 Human sec
23	611	100.0	117	6	AAW58977 Human sec
24	611	100.0	117	6	AAW92355 Novel hum

ALIGNMENTS

RESULT 1

AAW87991
ID AAW87991 standard; protein; 117 AA.

XX AC AAW87991;

DT 07-APR-1999 (first entry)

XX Protein designated zsig33.

XX Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
nutrient absorption regulation; obesity; metabolic disorder.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Peptide 1..23
FT Protein /note= "signal peptide"

FT Protein 24..117
FT Protein /note= "mature protein"

XX WO9842840-A1.

XX 01-OCT-1998.

XX 23-MAR-1998; 98WO-US005620.

XX 24-MAR-1997; 97US-0041102P.

XX 24-MAR-1997; 97US-00822897.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Deisher TA;

XX WPI; 1999-070071/06.

XX N-PSDB; AAX04550.

XX Human polypeptide having homology to motilin, zsig33 - useful e.g. to
treat gastrointestinal motility disorders, obesity etc. and to identify
antagonists to treat gastrointestinal hypermotility.

XX Claim 13; Page 55-56; 69pp; English.

XX The present sequence represents a protein designated Zsig33. The nucleic
acids are strongly expressed in stomach tissue. The polypeptide (or
allelic variants/orthologs) can be used to stimulate gastric motility,
measured as increased transit time or gastric emptying of an ingested

1.6
1.6

CC substance in mammals. The products are used to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes/acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
 CC absorption regulation. Zsig33 polypeptides may also be important
 CC neurologically, since the family of gut-brain peptides to which the
 CC homologous protein motilin belongs has been associated with neurological
 CC and CNS functions. They may therefore be used e.g. to regulate satiety or
 CC treat obesity and other metabolic disorders where neurological feedback
 CC modulates nutritional absorption. They are useful to identify zsig33
 CC agonists, antagonists and ligands and to produce antibodies
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 2; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKSKPKLQPRALAGWLRLPE 60
 DB 1 MPSPTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKSKPKLQPRALAGWLRLPE 60
 QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQVQHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQVQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 2
 AAY87236
 ID AAY87236 standard; protein; 117 AA.
 XX
 AC AAY87236;
 XX
 DT 11-MAY-2000 (first entry)
 DE Human signal peptide containing protein HSP-13 SEQ ID NO:13.
 XX
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
 KW antischmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US014484.
 XX
 PR 26-JUN-1998; 98US-0090762P.
 PR 31-JUL-1998; 98US-0094983P.
 PR 01-OCT-1998; 98US-0102686P.
 PR 11-DEC-1998; 98US-0112129P.
 XX
 PA (INCY-) INCYTE PHARM INC.

XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 DR WPI: 2000-160673/14.
 DR N-PSDB; AAZ98121.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
 PT disease.
 XX

PS Claim 1; Page 168-169; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
 CC used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
 CC or ribozyme therapeutics, for detecting related sequences or genetic
 CC variations, and for chromosomal mapping. HSP are also used to raise
 CC specific antibodies (Ab) and to screen for agonists and antagonists
 CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
 CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
 CC competitive drug screens, and for purification of HSP from natural
 CC sources
 XX
 SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 3; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKSKPKLQPRALAGWLRLPE 60
 DB 1 MPSPTVCSSLLLLGMLDLAMAGSSFLSPHQVQQRKSKPKLQPRALAGWLRLPE 60
 QY 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQVQHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQVQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 3
 AAB20101
 ID AAB20101 standard; protein; 117 AA.
 XX
 AC AAB20101;
 XX
 DT 23-APR-2001 (first entry)
 DE Zsig33 protein.
 XX
 KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
 KW nutritional absorption modulator; growth hormone secretagogue; therapy;
 KW human.
 XX
 OS Homo sapiens.
 FH Key
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..117
 FT /label= Mature_protein
 FT Peptide 24..34
 FT /label= SGIP_peptide
 FT /note= "this peptide is claimed in Claim 1"
 XX
 PN WO200100830-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US018306.
 XX


```
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB; AAI58046.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 3; SEQ ID NO 2035; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAI3642-AAI42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 611; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPSPTVCSSLILGLMLDLAMAGSFLSPHQVQQRKSKPKPKLQPRALAGWLRLPE 60
DB 1 MPSPTVCSSLILGLMLDLAMAGSFLSPHQVQQRKSKPKPKLQPRALAGWLRLPE 60
QY 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
DB 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
RESULT 6
AAB60511
ID AAB60511 standard; protein; 117 AA.
XX
XX AAB60511;
AC AAB60511;
XX
XX 24-APR-2001 (first entry)
DT
DE Human ghrelin preproprotein, SEQ ID NO:5.
XX
XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW calcium concentration elevation; infant growth disorder;
KW growth hormone deficiency.
XX
XX Homo sapiens.
OS
XX
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PN WO200107475-A1.
XX
PD 01-FEB-2001.
XX
XX 24-JUL-2000; 2000WO-JP004907.
XX
XX 23-JUL-1999; 99JP-00210002.
PR 29-NOV-1999; 99JP-00338841.
PR 26-APR-2000; 2000JP-00126623.
XX
XX (KANG/) KANGAWA K.
XX
XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
PI WPI: 2001-159704/16.
DR N-PSDB; AAF59645.
XX
XX New peptide compounds which induce growth hormone secretion and elevate
PT cell calcium concentrations, useful in treatment and diagnosis of infant
PT growth disorders.
XX
XX Claim 3; Page 182; 210pp; Japanese.
XX
XX The invention relates to a novel peptide compound or its salt which
CC induces the secretion of growth hormone and/or elevates calcium ion
CC concentration in cells. The peptides are ghrelin homologues and are
CC characterised in that at least one amino acid has been substituted by a
CC modified amino acid and/or a non-amino acid compound. The invention also
CC encompasses the unmodified peptides; the DNA encoding the peptides;
CC vectors and host cells comprising such DNA; a method of producing the
CC peptides comprising recombinant production, optionally followed by
CC chemical modification; an antibody specific for a peptide of the
CC invention; and an assay and kit for detecting the peptides. The peptides
CC of the invention are useful for treating and/or diagnosing diseases
CC caused by a deficiency in growth hormone expression or activity. In
CC particular, they are useful for promoting infant growth due to growth
CC hormone deficiency. The compounds of the invention are safe with no
CC accompanying side effects. The present sequence represents a ghrelin-type
CC growth hormone secretagogue (GHS) precursor protein of the invention
XX
XX SQ Sequence 117 AA;
Query Match 100.0%; Score 611; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPSPTVCSSLILGLMLDLAMAGSFLSPHQVQQRKSKPKPKLQPRALAGWLRLPE 60
DB 1 MPSPTVCSSLILGLMLDLAMAGSFLSPHQVQQRKSKPKPKLQPRALAGWLRLPE 60
QY 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
DB 61 DGGQAEAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
RESULT 7
ABB78319
ID ABB78319 standard; protein; 117 AA.
XX
XX ABB78319;
AC ABB78319;
XX
XX 05-DEC-2002 (first entry)
DT
DE Amino acid sequence of a human zsig33.
XX
XX Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1..23
FT Peptide /note= "signal peptide"
FT Protein 24..119
```


FT XX /note= "mature protein"

PN US6420521-B1.

XX 16-JUL-2002.

PD 30-JUN-2000; 2000US-00608810.

PF 30-JUN-1999; 99US-0141592P.

PR (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

PI WPI; 2002-634794/68.

XX N-PSDB; ABV72214.

DR New Short Gastrointestinal Peptide, which has homology to motilin, useful

PT for preventing, diagnosing and treating gastrointestinal disorders.

XX Disclosure; Col 39-40; 23pp; English.

PS The present sequence represents human zsig33. The specification describes

CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.

CC SGIP has homology to motilin. The SGIP peptide may be used in the

CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate SGIP expression. For example, SGIP may be used to treat

CC disorders associated with decreased expression by rectifying mutations or

CC deletions in a patient's genome that affect the activity of SGIP by

CC expressing inactive proteins or to supplement the patients own production

CC of SGIP. SGIP may also be used as an antigen in the production of

CC antibodies against SGIP and in assays to identify modulators of SGIP

CC expression and activity. The anti-SGIP antibodies, agonists and

CC antagonists may also be used to regulate expression and activity. The

CC anti-SGIP antibodies may also be used as diagnostic agents for detecting

CC the presence of SGIP in samples

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 5; Length 117;

Best Local Similarity 100.0%; Pred. No. 4e-59;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLLLGMLWLDLDMAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRPE 60

Db 1 MPSPTVCSLLLLGMLWLDLDMAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRPE 60

Qy 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 8

AAE23838

ID AAE23838 standard; protein; 117 AA.

XX AAE23838;

AC AAE23838;

XX 10-SEP-2002 (first entry)

DT Human zsig33 protein.

DE Human; zsig33-like peptide; gastric contractility; nutrient uptake;

XX growth hormone; digestive enzyme; restorative therapy; gene therapy;

XX protein therapy; gastrointestinal; endocrine; anabolic.

OS Homo sapiens.

XX US2002055156-A1.

PN 09-MAY-2002.

PD 10-MAY-2001; 2001US-00853253.

PF 11-MAY-2000; 2000US-0203300P.

XX (JASP/) JASPERS S R.

PA (SHEP/) SHEPPARD P O.

PA (DEIS/) DEISHER T A.

PA (BISH/) BISHOP P D.

PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;

XX WPI; 2002-443750/47.

DR N-PSDB; AAD38238.

XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

PT contractility, nutrient uptake, growth hormones and/or secretion of

PT digestive/pancreatic enzymes and hormones.

XX Disclosure; Page 27; 34pp; English.

PS The invention relates to zsig33-like peptides and their corresponding

CC nucleic acids and methods for modulating gastric contractility, nutrient

CC uptake, growth hormones, secretion of digestive enzymes and hormones. The

CC sequences of the invention are used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate zsig33 expression.

CC The nucleic acids of the invention and their complements are used as DNA

CC probes in diagnostic assays to detect and quantitate the presence of

CC similar nucleic acids in samples, and therefore which patients may be in

CC need of restorative therapy. The zsig33 peptides are used as antigens in

CC the production of antibodies against zsig33 and in assays to identify

CC modulators of zsig33 expression and activity. The anti-zsig33 antibodies

CC and antagonists are used to down regulate expression and activity. The

CC anti-zsig33 antibodies are also used as diagnostic agents for detecting

CC the presence of zsig33 in samples (e.g. by enzyme linked immunosorbent

CC assay (ELISA)). The peptides and nucleic acids of the invention are used

CC to modulate gastric contractility, nutrient uptake, growth hormones, the

CC secretion of digestive enzymes and hormones, and/or secretion of enzymes

CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy

CC and zsig33-like peptide is used in protein therapy. The present sequence

CC is human zsig33 protein

XX SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 5; Length 117;

Best Local Similarity 100.0%; Pred. No. 4e-59;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLLLGMLWLDLDMAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRPE 60

Db 1 MPSPTVCSLLLLGMLWLDLDMAGSSFLSPHQVQQRKSKPKPKLQPRALAGWLRPE 60

Qy 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 9

AAE15883

ID AAE15883 standard; protein; 117 AA.

XX AAE15883;

AC AAE15883;

XX 26-MAR-2002 (first entry)

DT Human zsig33 protein.

DE Human; zsig33-like peptide; zsig33LP; immunity; developmental process;

XX infection; human immunodeficiency virus; vaccine; antihypoglycaemic;

XX adsorption enhancer; gastrointestinal disease; growth related disease;

XX inflammation; gene therapy; growth regulation; blood vessel formation;

XX HIV; zsig33 protein.

XX Homo sapiens.

OS Homo sapiens.

XX

FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /label= Signal_peptide
FT 24..117
FT /note= "Human mature zsig33 protein"
XX
XX WO200187933-A2.
XX
XX
XX 22-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-US015091.
XX
XX 11-MAY-2000; 2000US-00569271.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
XX WPI: 2002-082982/11.
XX N-PSDB; AAD25759.
XX
XX New polypeptides, useful for modulating gastric contractility, nutrient
PT uptake, pancreatic secretion of hormones, digestive enzymes and treating
PT gastrointestinal and growth related diseases, comprises zsig33-like
PT peptides.
XX
XX Disclosure; Page 80-81; 89pp; English.
XX
XX The invention relates to zsig33-like peptides (ZS33LP) including zsig33-
CC linker, zsig33-beta, zsig33-gamma, zsig33-delta and zsig33-epsilon
CC peptides and nucleic acid molecules encoding such zsig33-like peptides.
CC ZS33LP peptides activate the immune system in boosting immunity to
CC infectious diseases, treating immunocompromised patients such as human
CC immunodeficiency virus (HIV) patients, in improving vaccines and in
CC treatment of bacterial, viral, protozoal and fungal infections. Peptides
CC of the invention are used to identify and isolate receptors involved in
CC growth regulation in the liver, blood vessel formation and other
CC developmental processes. They are useful for evaluating functions of
CC hypothalamus-pituitary-adrenal axis, to modulate growth and/or
CC differentiation of tumour cells, as additives to anti- hypoglycaemic
CC preparations containing glucose and as adsorption enhancers for oral
CC drugs which require fast nutrient action and to stimulate glucose-induced
CC insulin release. They are also useful as research reagents for the
CC expansion, differentiation, growth factor and hormone secretion and/or
CC cell-cell interactions of tissues associated with gastrointestinal
CC system, brain and central nervous system. These molecules are useful for
CC treating dysfunction associated with contractile tissues or to suppress
CC or enhance contractility in vivo and to treat gastrointestinal and growth
CC related diseases. ZS33LP peptides, nucleic acids and/or antibodies are
CC useful for treating disorders associated with gastrointestinal
CC contractility, secretion of digestive enzymes, hormone and acids,
CC secretion of hormones in the pancreas and/or brain, gastrointestinal
CC motility, recruitment of digestive enzymes, inflammation and regulation
CC of nutrient absorption. Sequences of the invention are useful in gene
CC therapy. The present sequence is human zsig33 protein
XX
XX Sequence 117 AA;
SQ

Query Match 100.0%; Score 611; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSGTVCSSLLLLGLMGLDLAMAGSFLSPHEHQVQQRKESKPPAKLQPRALAGWLRLPE 60
DQ 1 MSPSGTVCSSLLLLGLMGLDLAMAGSFLSPHEHQVQQRKESKPPAKLQPRALAGWLRLPE 60
QY 61 DGGQAGAGDELEVRNPDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
DQ 61 DGGQAGAGDELEVRNPDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 10
ABU58046

ID ABU58046 standard; protein; 117 AA.
XX
AC ABU58046;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #78.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.

PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090542P.
PR 24-JUN-1998; 98US-0090557P.
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PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 26-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0096962P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.

PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100858P.
PR 07-OCT-1998; 98US-0100858P.
PR 01-DEC-1998; 98US-0100858P.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99US-01000106.
PR 08-MAR-1999; 99US-01000106.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99US-0123957P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149386P.
PR 15-SEP-1999; 99US-0149386P.
PR 15-SEP-1999; 99US-0149386P.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99US-0158663P.
PR 01-DEC-1999; 99US-0158663P.
PR 01-DEC-1999; 99US-0158663P.
PR 16-DEC-1999; 99US-0158663P.
PR 20-DEC-1999; 99US-0158663P.
PR 05-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000376.
PR 11-FEB-2000; 2000US-0003565.
PR 18-FEB-2000; 2000US-0004341.
PR 22-FEB-2000; 2000US-0004414.
PR 24-FEB-2000; 2000US-0004914.
PR 02-MAR-2000; 2000US-0005004.
PR 10-MAR-2000; 2000US-0005841.
PR 15-MAR-2000; 2000US-0006319.
PR 20-MAR-2000; 2000US-0006884.
PR 30-MAR-2000; 2000US-0007377.
PR 30-MAR-2000; 2000US-0008439.
PR 15-MAY-2000; 2000US-013358.
PR 17-MAY-2000; 2000US-013705.
PR 22-MAY-2000; 2000US-014042.
PR 30-MAY-2000; 2000US-014941.
PR 02-JUN-2000; 2000US-015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000US-020710.
PR 11-AUG-2000; 2000US-022031.
PR 23-AUG-2000; 2000US-023352.
PR 24-AUG-2000; 2000US-023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 100.0%; Score 611; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQRVQQRKSKKPPAKLQPRALAGWLPE 60
Db 1 MPSPGTVCSSLLLLGMLDLAMAGSSFLSPHQRVQQRKSKKPPAKLQPRALAGWLPE 60
Qy 61 DGGQAECADELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAECADELEVRFNAPFDVGIKLSGVYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 11
ABUS9124
ID ABUS9124 standard; protein; 117 AA.
XX
AC ABUS9124;

XX DT 28-APR-2003 (first entry)

XX DE Novel human secreted or transmembrane protein PRO1066.

XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;

XX KW cardiac insufficiency disorder; cancer; tumour; immune response;

XX KW adrenal cortical capillary endothelial growth; c-fos induction;

XX KW vascular endothelial growth factor inhibition; VEGF inhibition;

XX KW endothelial cell growth inhibitor; T-lymphocytes stimulation;

XX KW retinal neurons cell survival; rod photoreceptor cell survival;

XX KW retinal disorder; retinitis pigmentosa; kidney disorder;

XX KW mammalian kidney mesangial cell proliferation; Berger disease;

XX KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;

XX KW chondrocyte redifferentiation; sports injury; arthritis.

OS Homo sapiens.

XX US2002132252-A1.

XX PN 19-SEP-2002.

XX PD 14-NOV-2001; 2001US-00990442.

XX PF 16-JUN-1997; 97US-0049787P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 05-NOV-1997; 97WO-US020069.

XX PR 12-NOV-1997; 97US-0065186P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 24-NOV-1997; 97US-0066770P.

XX PR 25-FEB-1998; 98US-0075945P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 28-APR-1998; 98US-0083322P.

XX PR 07-MAY-1998; 98US-0084600P.

XX PR 28-MAY-1998; 98US-0087106P.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 02-JUN-1998; 98US-0087759P.

XX PR 03-JUN-1998; 98US-0087827P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088026P.

XX PR 04-JUN-1998; 98US-0088028P.

XX PR 04-JUN-1998; 98US-0088029P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 04-JUN-1998; 98US-0088033P.

XX PR 04-JUN-1998; 98US-0088326P.

XX PR 05-JUN-1998; 98US-0088167P.

XX PR 05-JUN-1998; 98US-0088202P.

XX PR 05-JUN-1998; 98US-0088212P.

XX PR 05-JUN-1998; 98US-0088217P.

XX PR 09-JUN-1998; 98US-0088655P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088738P.

XX PR 10-JUN-1998; 98US-0088742P.

XX PR 10-JUN-1998; 98US-0088810P.

XX PR 10-JUN-1998; 98US-0088824P.

XX PR 10-JUN-1998; 98US-0088826P.

XX PR 11-JUN-1998; 98US-0088858P.

XX PR 11-JUN-1998; 98US-0088861P.

XX PR 11-JUN-1998; 98US-0088876P.

XX PR 12-JUN-1998; 98US-0089105P.

XX PR 16-JUN-1998; 98US-0089440P.

XX PR 16-JUN-1998; 98US-0089512P.

XX PR 16-JUN-1998; 98US-0089514P.

XX PR 17-JUN-1998; 98US-0089532P.

XX PR 17-JUN-1998; 98US-0089538P.

XX PR 17-JUN-1998; 98US-0089598P.

XX PR 17-JUN-1998; 98US-0089599P.

XX PR 17-JUN-1998; 98US-0089600P.

XX PR 17-JUN-1998; 98US-0089603P.

XX PR 18-JUN-1998; 98US-0089801P.

XX PR 18-JUN-1998; 98US-0089907P.

PR 18-JUN-1998; 98US-0089908P.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US012252.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 06-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

PR 30-MAR-2000; 2000WO-US008439.

PR 15-MAY-2000; 2000WO-US013358.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

PR 28-AUG-2001; 2001US-00941992.

XX (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;

XX WPI; 2003-247083/24.

XX N-PSDB; ABX80294.

XX PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1345

XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes

XX are therapeutically useful for enhancing immune response and in cancer

XX treatments.

XX Claim 12; Fig 186; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO

XX polypeptides are useful in detecting PRO polypeptides in a sample, in

XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and

XX in modulating at least one biological activity of a cell expressing a PRO

XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus

XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186

XX stimulate adrenal cortical capillary endothelial growth, and PRO536,

XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO819, PRO1126,

XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus

XX useful for treating conditions or disorders where angiogenesis would be

CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with,
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein

XX Sequence 117 AA;

Query Match 100.0%; Score 611; DB 6; Length 117;

Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLPQALAGWLPE 60

Db 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQQRKESKPPAKLPQALAGWLPE 60

Qy 61 DGGQAEAGDELEVRFNAPFDVGIKLGVQYQHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAEAGDELEVRFNAPFDVGIKLGVQYQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 12

ABU82636

ID ABU82636 standard; protein; 117 AA.

XX AC ABU82636;

XX DT 26-JUN-2003 (first entry)

XX DE Human secreted/transmembrane protein PRO1066.

XX KW Human; PRO; secreted protein; transmembrane protein;
XX KW cardiac insufficiency disorders; angiogenesis; wound healing;
XX KW cancerous tumour; immune response; retinal disorder; sight loss;
XX KW retinitis pigmentosa; age-related macular degeneration; AMD;
XX KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
XX KW Crohn's disease; sports injury; arthritis.

OS Homo sapiens.

XX US2003032023-A1.

XX PD 13-FEB-2003.

XX PF 14-NOV-2001; 2001US-00990711.

XX PR 16-JUN-1997; 97US-0049787P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 05-NOV-1997; 97WO-US020069.

XX PR 12-NOV-1997; 97US-0065186P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 24-NOV-1997; 97US-0066770P.

XX PR 25-FEB-1998; 98US-0075945P.

XX PR 20-MAR-1998; 98US-0078910P.

XX PR 28-APR-1998; 98US-0083322P.

XX PR 07-MAY-1998; 98US-0084600P.

XX PR 28-MAY-1998; 98US-0087106P.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
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PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
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PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
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PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
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PR 25-JUN-1998; 98US-0090695P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
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PR 02-JUL-1998; 98US-0091628P.
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PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.

PR 07-JUL-1998;	98US-0091982P.	PR 11-FEB-2000;	2000WO-US003565.
PR 09-JUL-1998;	98US-0092182P.	PR 18-FEB-2000;	2000WO-US004341.
PR 10-JUL-1998;	98US-0092472P.	PR 22-FEB-2000;	2000WO-US004114.
PR 20-JUL-1998;	98US-0093339P.	PR 24-FEB-2000;	2000WO-US004914.
PR 30-JUL-1998;	98US-0094651P.	PR 24-FEB-2000;	2000WO-US005004.
PR 04-AUG-1998;	98US-0095282P.	PR 02-MAR-2000;	2000WO-US005841.
PR 04-AUG-1998;	98US-0095285P.	PR 10-MAR-2000;	2000WO-US006319.
PR 04-AUG-1998;	98US-0095301P.	PR 15-MAR-2000;	2000WO-US006884.
PR 04-AUG-1998;	98US-0095302P.	PR 20-MAR-2000;	2000WO-US007377.
PR 04-AUG-1998;	98US-0095318P.	PR 30-MAR-2000;	2000WO-US008439.
PR 04-AUG-1998;	98US-0095321P.	PR 15-MAY-2000;	2000WO-US013358.
PR 04-AUG-1998;	98US-0095325P.	PR 17-MAY-2000;	2000WO-US013705.
PR 10-AUG-1998;	98US-0095916P.	PR 22-MAY-2000;	2000WO-US014042.
PR 10-AUG-1998;	98US-0095929P.	PR 30-MAY-2000;	2000WO-US014941.
PR 10-AUG-1998;	98US-0096012P.	PR 02-JUN-2000;	2000WO-US015264.
PR 11-AUG-1998;	98US-0096143P.	PR 23-JUN-2000;	2000US-0213637P.
PR 11-AUG-1998;	98US-0096146P.	PR 28-JUL-2000;	2000WO-US020710.
PR 12-AUG-1998;	98US-0096329P.	PR 11-AUG-2000;	2000WO-US022031.
PR 17-AUG-1998;	98US-0096757P.		
PR 17-AUG-1998;	98US-0096766P.	Query Match	100.0%; Score 611; DB 6; Length 117;
PR 17-AUG-1998;	98US-0096768P.	Best Local Similarity	100.0%; Pred. No. 4e-59;
PR 17-AUG-1998;	98US-0096773P.	Matches 117; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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PR 17-AUG-1998;	98US-0096891P.	DB 1	MPSPGTVCSSLLLLGMLWLDLAWAGSSFLSPHQRVQQRKSKPPAKLPRLAGWLREP 60
PR 17-AUG-1998;	98US-0096894P.		
PR 17-AUG-1998;	98US-0096895P.	QY 61	DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
PR 17-AUG-1998;	98US-0096897P.	DB 61	DGGQAGAEDELEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
PR 18-AUG-1998;	98US-0096949P.		
PR 18-AUG-1998;	98US-0096950P.		
PR 18-AUG-1998;	98US-0096959P.		
PR 18-AUG-1998;	98US-0096960P.		
PR 18-AUG-1998;	98US-0097022P.	RESULT 13	
PR 19-AUG-1998;	98US-0097141P.	ABOI7836	
PR 20-AUG-1998;	98US-0097218P.	ID ABOI7836	standard; protein; 117 AA.
PR 24-AUG-1998;	98US-0097661P.	XX	
PR 24-AUG-1998;	98US-0097952P.	AC ABOI7836;	
PR 26-AUG-1998;	98US-0097954P.	XX	
PR 26-AUG-1998;	98US-0097955P.	DT 26-AUG-2003	(first entry)
PR 26-AUG-1998;	98US-0097971P.	XX	
PR 26-AUG-1998;	98US-0097974P.	DE	Novel human secreted and transmembrane protein PRO1065.
PR 26-AUG-1998;	98US-0097978P.	XX	
PR 26-AUG-1998;	98US-0097979P.	XX	
PR 26-AUG-1998;	98US-0097986P.	KW	Human; secreted and transmembrane protein; PRO; antiinflammatory;
PR 26-AUG-1998;	98US-0098014P.	KW	antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
PR 31-AUG-1998;	98US-0098525P.	KW	antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
PR 16-SEP-1998;	98US-0100634P.	KW	TNF-alpha release; cell proliferation; cell differentiation;
PR 16-SEP-1998;	98WO-US019330.	KW	gene expression modulator; proteoglycan release; cytokine release;
PR 17-SEP-1998;	98US-0100858P.	KW	tumour; inflammatory disease; organ failure; atherosclerosis;
PR 17-SEP-1998;	98WO-US019437.	KW	cardiac injury; infertility; birth defect; premature aging; AIDS;
PR 07-OCT-1998;	98WO-US021141.	KW	acquired immunodeficiency syndrome; cancer; diabetic complication;
PR 01-DEC-1998;	98WO-US025108.	KW	chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
PR 22-DEC-1998;	98US-0113296P.	XX	bioreactor; tissue typing.
PR 05-JAN-1999;	99WO-US000106.	XX	
PR 08-MAR-1999;	99WO-US005028.	OS	Homo sapiens.
PR 12-MAR-1999;	99US-0123957P.	XX	
PR 02-JUN-1999;	99WO-US012252.	PN	US2003032156-A1.
PR 23-JUN-1999;	99US-0141037P.	XX	
PR 07-JUL-1999;	99US-0143048P.	PD	13-FEB-2003.
PR 20-JUL-1999;	99US-0144758P.	XX	
PR 26-JUL-1999;	99US-014568P.	PF	06-MAY-2002; 2002US-00140474.
PR 28-JUL-1999;	99US-0146222P.	XX	
PR 17-AUG-1999;	99US-0149396P.	PR 31-MAR-1997;	97WO-US005230.
PR 15-SEP-1999;	99WO-US021090.	PR 12-JUN-1998;	98WO-US012456.
PR 15-SEP-1999;	99WO-US021547.	PR 14-JUL-1998;	98WO-US014552.
PR 08-OCT-1999;	99US-0158663P.	PR 28-AUG-1998;	98WO-US017888.
PR 30-NOV-1999;	99WO-US028313.	PR 10-SEP-1998;	98WO-US018824.
PR 01-DEC-1999;	99WO-US028301.	PR 14-SEP-1998;	98WO-US019093.
PR 01-DEC-1999;	99WO-US028634.	PR 14-SEP-1998;	98WO-US019094.
PR 16-DEC-1999;	99WO-US030095.	PR 14-SEP-1998;	98WO-US019177.
PR 20-DEC-1999;	99WO-US030911.	PR 16-SEP-1998;	98WO-US019330.
PR 05-JAN-2000;	2000WO-US000219.	PR 17-SEP-1998;	98WO-US019437.
PR 06-JAN-2000;	2000WO-US000376.	PR 07-OCT-1998;	98WO-US021141.
		PR 29-OCT-1998;	98WO-US022991.

AC ABU60555;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #108.
XX
KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-0092598.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083222P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
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PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-FEB-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001WO-US021932.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen MB, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;
PI Zhang Z;
XX
WI; 2003-288106/28.
DR N-PSDB; ABX90272.
XX
DR New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 12; Fig 186; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX


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SQ Sequence 117 AA;
Query Match 100.0%; Score 611; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSPTVCSLLILGLMLDLAMAGSSFLSPHQRVQQRKESKPPAKLQPRALAGWLKPE 60
Db 1 MPSPTVCSLLILGLMLDLAMAGSSFLSPHQRVQQRKESKPPAKLQPRALAGWLKPE 60

Qy 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 15
ABU13937
ID ABU13937 standard; protein; 117 AA.
XX
AC ABU13937;
XX
DT 26-FEB-2003 (first entry)
XX
DE Human PRO1066 polypeptide.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW Genetic disorder; antibacterial; immunosuppressive.
XX
OS Homo sapiens.
XX
PN US2002103125-A1.
XX
PD 01-AUG-2002.
XX
PF 20-NOV-2001; 2001US-00989731.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.

12-JUN-1998; 98US-0089105P.
16-JUN-1998; 98US-0089440P.
16-JUN-1998; 98US-0089512P.
17-JUN-1998; 98US-0089514P.
17-JUN-1998; 98US-0089532P.
17-JUN-1998; 98US-0089538P.
17-JUN-1998; 98US-0089598P.
17-JUN-1998; 98US-0089599P.
17-JUN-1998; 98US-0089600P.
18-JUN-1998; 98US-0089653P.
18-JUN-1998; 98US-0089801P.
18-JUN-1998; 98US-0089907P.
18-JUN-1998; 98US-0089908P.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
07-OCT-1998; 98WO-US021141.
01-DEC-1998; 98WO-US025108.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
02-JUN-1999; 99WO-US012252.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
06-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
23-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.

(GETH ) GENENTECH LTD.
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI;
Zhang Z;
WPI; 2003-102117/09.
N-PSDB; ABX64118.
Novel secreted and transmembrane polypeptide for modulating biological
activity of cell expressing the polypeptide, identifying agonists or
antagonists of polypeptide, and as molecular weight markers.
Claim 12; Fig 186; 649pp; English.
PS
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XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for for
 CC identifying agonists or antagonists. The polynucleotide sequences
 CC encoding PRO polypeptides are useful as hybridisation probes, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC in the preparation of PRO polypeptides, for generating transgenic animals
 CC or knockout animals, to construct hybridisation probes for mapping the
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome markers, and for generating probes for PCR,
 CC Northern analysis, Southern analysis and Western analysis. ABU13860-
 CC ABU14006 represent the human PRO polypeptides of the invention. Note: The
 CC sequence data for this patent was obtained in electronic format directly
 CC from the USPTO web site at seqdata.uspto.gov/psipsIDEntry.html
 XX

SQ Sequence 117 AA;

Query Match 100.0%; Score 611; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4e-59;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPSPGTVCSSLLLLGMLWLDLDMAGSSFLSPHQVQQRKESKPPAKLOPRALAGWLRPE 60
 Db |||||
 1 MPSPGTVCSSLLLLGMLWLDLDMAGSSFLSPHQVQQRKESKPPAKLOPRALAGWLRPE 60
 QY 61 DGGQAGGADELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
 Db |||||
 61 DGGQAGGADELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117

Search completed: April 10, 2006, 17:28:37
 Job time : 67.646 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:29:03 ; Search time 12.1118 Seconds
(without alignments)
929.454 Million cell updates/sec

Title: US-09-718-803A-2
Perfect score: 611
Sequence: 1 MPSPGTVCSSLLGLMLDL.....LGKFLQDLWEEAKEAPADK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	100.0	117	1 A59316	ghrelin precursor
2	518	84.8	117	1 B59316	ghrelin precursor
3	88.5	14.5	115	1 A33323	motilin precursor
4	86	14.1	119	1 MSPG	motilin precursor
5	79	12.9	1234	2 T30160	hypothetical prote
6	75.5	12.4	410	2 C84205	hypothetical prote
7	73.5	12.0	709	2 D82825	conserved hypothet
8	72.5	11.9	115	2 JC6511	motilin precursor
9	72.5	11.9	482	1 S03904	platelet-derived e
10	72.5	11.9	922	2 G83109	probable two-compo
11	72	11.8	147	2 T09722	histone H2B1 - upl
12	71	11.6	299	2 B36134	RepC protein - Esc
13	70	11.5	840	2 F90788	probable outer mem
14	70	11.5	840	2 G85648	probable usher pro
15	69	11.3	411	2 S47436	flagellar antigen
16	69	11.3	792	2 JC7122	protein kinase (EC
17	69	11.3	2273	2 T46477	calcium channel BI
18	69	11.3	2424	2 T46480	calcium channel BI
19	68.5	11.2	133	1 S24315	motilin precursor
20	68.5	11.2	340	2 S53763	homeotic protein H
21	68.5	11.2	330	2 AC0414	probable exported
22	68	11.1	533	2 A82292	beta-hexosaminidas
23	68	11.1	409	2 D87426	cyclopropane-fatty
24	67.5	11.0	270	2 E87408	hypothetical prote
25	67.5	11.0	416	2 T38428	T-complex protein
26	67.5	11.0	938	2 A13417	[glutamate-ammonia
27	67	11.0	233	2 T41263	hypothetical prote
28	67	11.0	2212	2 A41098	calcium channel pr
29	66.5	10.9	385	2 F70591	probable kefB prot

30	66.5	10.9	485	2	C75460	hypothetical prote
31	66.5	10.9	575	2	F86639	hypothetical prote
32	66.5	10.9	992	2	T08772	hypothetical prote
33	66.5	10.9	1018	2	T43168	hypothetical prote
34	66.5	10.9	1171	2	A50150	DNA-directed DNA p
35	66	10.8	247	2	S58394	myelin/oligodendro
36	66	10.8	770	2	A54444	DNA-binding protei
37	66	10.8	770	2	T49508	ISGF3 p91-related
38	66	10.8	922	2	D75615	excinuclease ABC c
39	65.5	10.7	262	2	D71068	probable pseudouri
40	65.5	10.7	334	2	S39870	transaldolase (EC
41	65.5	10.7	491	2	H97088	protein containing
42	65.5	10.7	627	2	T19542	hypothetical prote
43	65.5	10.7	692	2	AE0745	flagellar biosynth
44	65.5	10.7	692	2	B55546	flagellar biosynth
45	65.5	10.7	1065	2	B69795	acriflavin resista

ALIGNMENTS

RESULT 1

A59316
Ghrelin precursor - human
N;Alternate names: preproghrelin
C;Species: Homo sapiens (man)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A;Accession: A59316
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-117 <KOJ>
A;Cross-references: UNIPROT:Q9UBU3; UNIPARC:UPI00000362D3; GB:AB029434; NID:g6691571; E
A;Experimental source: tissue stomach endocrine cells
A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (gro
C;Superfamily: motilin
C;Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <MAT>
F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 611; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-54;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQQRKSKPPAKLOPRALAGWLPE	60
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Qy	61	DGQGAEGAELEVRFNAPDVGKLSGVQVQHSQALGKFLQDLWEEAKEAPADK	117
Db	61	DGQGAEGAELEVRFNAPDVGKLSGVQVQHSQALGKFLQDLWEEAKEAPADK	117

RESULT 2

B59316
Ghrelin precursor - rat
N;Alternate names: preproghrelin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C;Accession: B59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A;Accession: B59316
A;Status: not compared with conceptual translation

A:Molecule type: mRNA; protein
A:Residues: 1-117 <XOU>
A:Cross-references: UNIPROT:Q9QYH7; UNIPARC:UPI000012B411; GB:AB029433; NID:g6691569; PID:1-117
A:Experimental source: strain SD; tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the stomach
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 84.8%; Score 518; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 4.1e-45;
Matches 97; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MSPGTCVCSLLGLMLDLAMAGSSFLSPHQVQQRKESKKPPAKLQPRALAGWLRAPE 60
Db 1 MVSSATICSLLGLMLMDMAMAGSFLSPHQVQQRKESKKPPAKLQPRALAGWLRAPE 60

QY 61 DGGQAEAGAELEVRNPFDFVGIKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DRGQAEAEAELEIRNPFDFVGIKLSGAQYQHQHGRALGKFLQDILWEEVKEAPANK 117

RESULT 3
A33323
motilin precursor - human
N:Contains: motilin; promotilin
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
A:Accession: A33323; S04489; S00156; A30329
R:Daikh, D.I.; Douglass, J.O.; Adelman, J.P.
DNA 8, 615-621, 1989
A:Title: Structure and expression of the human motilin gene.
A:Reference number: A33323; MUID:90091748; PMID:2574660
A:Accession: A33323
A:Molecule type: DNA
A:Residues: 1-115 <DAL>
A:Cross-references: UNIPROT:P12872; UNIPARC:UPI000012F3B4; GB:M30277; GB:M30278; GB:M30279
A:Note: the authors translated the codon CAG for residue 93 as Glu
R:Yano, H.; Seino, Y.; Fujita, J.; Yamada, Y.; Inagaki, N.; Takeda, J.; Bell, G.I.; Eddy
R:FSB Lett. 249, 248-252, 1989
A:Title: Exon-intron organization, expression, and chromosomal localization of the human motilin gene.
A:Reference number: S04489; MUID:89289989; PMID:2737284
A:Accession: S04489
A:Molecule type: DNA
A:Residues: 1-115 <YAN>
A:Cross-references: UNIPARC:UPI000012F3E4; EMBL:X15393; NID:g34691; PIDN:CAA33448.1; PID:1-115
R:Seino, Y.; Tanaka, K.; Takeda, J.; Takahashi, H.; Mitani, T.; Kurono, M.; Kayano, T.;
R:FSB Lett. 223, 74-76, 1987
A:Title: Sequence of an intestinal cDNA encoding human motilin precursor.
A:Reference number: S00156; MUID:88030048; PMID:3666144
A:Accession: S00156
A:Molecule type: mRNA
A:Residues: 1-115 <SET>
A:Cross-references: UNIPARC:UPI000012F3E4; EMBL:Y00695; NID:g34716; PIDN:CAA68690.1; PID:1-115
R:Dea, D.; Boileau, G.; Poitras, P.; Lahate, R.G.
Gastroenterology 96, 695-703, 1989
A:Title: Molecular heterogeneity of human motilinlike immunoreactivity explained by the existence of two distinct genes.
A:Reference number: A30329; MUID:89121385; PMID:2914635
A:Accession: A30329
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14, A' 16-113, 115 <DEA>
A:Cross-references: UNIPARC:UPI000017352E
C:Comment: This peptide hormone stimulates small intestinal muscle.
C:Genetics:
A:Gene: GDB:MLN
A:Cross-references: GDB:120187; OMIM:158270
A:Map position: 6p21.3-6p21.3
A:Introns: 39/3; 78/3; 113/1

C:Superfamily: motilin
C:Keywords: hormone
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-114/Product: promotilin #status predicted <PMAT>
F:26-47/Product: motilin #status predicted <MAT>
F:50-115/Domain: carboxyl-terminal propeptide #status predicted <CTP>

Query Match 14.5%; Score 88.5; DB 1; Length 115;
Best Local Similarity 25.4%; Pred. No. 0.076;
Matches 31; Conservative 29; Mismatches 41; Indels 21; Gaps 5;

QY 1 MSPGTCVCSLLGLMLDLAMAGSS-----FLSPHQVQQRKESKKPPAKLQPRAL 53
Db 1 MVSRAVAALLVVHV-----AAMLASQTEAFVPIFYTGELQRMQEKERNKG-----QKXSL 51

QY 54 AGWLRPEDGGQAEGA-----EDELE-VRNPFDFVGIKLSGVQYQHSQALGKFLQDILWE 108
Db 52 SIVWQSSGEGPVDPAEPIREENENIKLTAPELIGRMVNSRQLEKYPATLEGLLSEMLPQ 111
QY 109 EA 110
Db 112 HA 113

RESULT 4
MSPG
motilin precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1984 #sequence revision 26-Jan-1996 #text_change 09-Jul-2004
A:Accession: A40932; A90748; A01578
R:Bond, C.T.; Milaver, G.; Godfrey, B.; Zimmerman, E.A.; Adelman, J.P.
Mol. Endocrinol. 2, 175-180, 1988
A:Title: Characterization of complementary deoxyribonucleic acid for precursor of porcine motilin.
A:Reference number: A40932; MUID:88288231; PMID:2456453
A:Accession: A40932
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <BON>
A:Cross-references: UNIPROT:P01307; UNIPARC:UPI0000362D4; GB:M31219; NID:g164589; PIDN:1-119
A:Note: the authors translated the codon AGC for residue 29 as Ile
R:Brown, J.C.; Cook, M.A.; Dryburgh, J.R.
Can. J. Biochem. 51, 533-537, 1973
A:Title: Motilin, a gastric motor activity stimulating polypeptide: the complete amino acid sequence of the porcine motilin.
A:Reference number: A90748; MUID:73184120; PMID:4708633
A:Accession: A90748
A:Molecule type: protein
A:Residues: 26-28, I', 30-38, E', 40-47 <BRO>
A:Cross-references: UNIPARC:UPI000017352C
A:Experimental source: duodenal mucosa
R:Schubert, H.; Brown, J.C.
Can. J. Biochem. 52, 7-8, 1974
A:Title: Correction to the amino acid sequence of porcine motilin.
A:Reference number: A90749; MUID:74138109; PMID:4856583
A:Accession: A90749
A:Molecule type: protein
A:Residues: 38-41 <SCH>
A:Cross-references: UNIPARC:UPI000017352D
R:Yajima, H.; Kai, Y.; Kawatani, H.
J. Chem. Soc. Commun. 1975, 159-160, 1975
A:Title: Synthesis of the docosa-peptide corresponding to the entire amino-acid sequence of the porcine motilin.
A:Reference number: A92756
A:Accession: A92756
A:Contents: annotation
A:Note: a 22-residue peptide having the sequence and biological activity of the natural porcine motilin.
R:Brown, J.C.; Mutt, V.; Dryburgh, J.R.
Can. J. Physiol. Pharmacol. 49, 399-405, 1971
A:Title: The further purification of motilin, a gastric motor activity stimulating polypeptide from the fundic gland area pouches.
A:Reference number: A90755; MUID:72043589; PMID:4941085
A:Accession: A90755
A:Contents: annotation
A:Note: motilin, injected intravenously into dogs, stimulates motor activity in both antroduodenal and ileocecal pouches.
C:Superfamily: motilin
C:Keywords: duodenal mucosa; hormone; stomach
F:1-25/Domain: signal sequence #status predicted <SIG>

RESULT 12

B36134
RepC protein - Escherichia coli plasmid TF-FC2
C:Species: Escherichia coli
C:Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 09-Jul-2004
C:Accession: B36134
R:Dorington, R.A.; Rawlings, D.E.
J. Bacteriol. 172, 5697-5705, 1990
A:Title: Characterization of the minimum replicon of the broad-host-range plasmid pTF-FC2
A:Reference number: A36134; MUID:91008941; PMID:2120189
A:Accession: B36134
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <DOR>
A:Cross-references: UNIPROT:Q03087; UNIPARC:UPI00000BE363; GB:M73777; GB:M35249; NID:g15
C:Genetics:
A:Genome: plasmid

Query Match 11.6%; Score 71; DB 2; Length 299;
Best Local Similarity 25.8%; Pred. No. 13;
Matches 25; Conservative 15; Mismatches 37; Indels 20; Gaps 4;

QY 32 HORVQQRKESK--KPPAKLQPRALAGWLRPEDGGQAE-----GAEDE-LEVRFN 77

DB 200 HTRINMAEVRKLETPARLLHQRLCGWDIDPGSKGAEDITLCGYVWPDAANDEAMKKRRQ 259

QY 78 APFDVGIKLGVOYQOHSQALGKFLQDILWEAKEAP 114

DB 260 TARKALVELAAVGTVNEYAKGK-----WEISRPNP 290

RESULT 13

F90788
probable outer membrane usher protein ECs1278 [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F90788
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90788
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840 <HAY>
A:Cross-references: UNIPROT:Q8XAP8; UNIPARC:UPI00000D06A2; GB:BA000007; PIDN:BA034701.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs1278
C:Superfamily: outer membrane usher protein fimD

Query Match 11.5%; Score 70; DB 2; Length 840;
Best Local Similarity 25.9%; Pred. No. 50;
Matches 30; Conservative 15; Mismatches 43; Indels 28; Gaps 5;

QY 3 SPGTVCSSLLILGMLWLDLWLAGSFLSPHQVQORVKESKPPAKLQPR-----LAG 55

DB 127 APG-ITSQTQLSQLRLDLSVPQSOLIS-----RPRGVVPPSELDTGASLAFMYIAN 177

QY 56 WLRPEDGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAK 111

DB 178 YYNVAYSGQNAHSQRLWASFN-----GINLGAWQYRQ-----LSNMTWDNDK 221

RESULT 14

G85648
probable usher protein Z1536 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85648
R:Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85648
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-840 <STO>
A:Cross-references: UNIPROT:Q8XAP8; UNIPARC:UPI000016575F; GB:AE005174; NID:g12514401;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1536
C:Superfamily: outer membrane usher protein fimD

Query Match 11.5%; Score 70; DB 2; Length 840;
Best Local Similarity 25.9%; Pred. No. 50;
Matches 30; Conservative 15; Mismatches 43; Indels 28; Gaps 5;

QY 3 SPGTVCSSLLILGMLWLDLWLAGSFLSPHQVQORVKESKPPAKLQPR-----LAG 55

DB 127 APG-ITSQTQLSQLRLDLSVPQSOLIS-----RPRGVVPPSELDTGASLAFMYIAN 177

QY 56 WLRPEDGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEAK 111

DB 178 YYNVAYSGQNAHSQRLWASFN-----GINLGAWQYRQ-----LSNMTWDNDK 221

RESULT 15

S47436

flagellar antigen - Trypanosoma brucei (fragment)
C:Species: Trypanosoma brucei

C:Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004

C:Accession: S47436

R:Imboden, M.; Mueller, N.; Hemphill, A.; Mattioli, X.V.Z.; Seebeck, T.

submitted to the EMBL Data Library, August 1994

A:Description: Repetitive proteins from the flagellar cytoskeleton of African Trypanosoma

A:Reference number: S47436

A:Accession: S47436

A:Molecule type: mRNA

A:Residues: 1-411 <IMB>

A:Cross-references: UNIPROT:Q26766; UNIPARC:UPI000007CBBB; EMBL:Z36281; NID:g530358; PI

A:Experimental source: strain stock TREU 1285

C:Superfamily: cytochrome-c oxidase

Query Match 11.3%; Score 69; DB 2; Length 411;

Best Local Similarity 30.2%; Pred. No. 29;

Matches 26; Conservative 16; Mismatches 28; Indels 16; Gaps 4;

QY 33 QRVQQRKESKPPAKLQPRALAGWLRPEDGGQAGAEDELEVRNAPFDVGIKLSGVQYQ 92

DB 317 EALDELEEPQAPAEQAQPEAVA---PE-GDIAVEALEELEEPQAP-----AEAQ 362

QY 93 QHSQALGKFLQDIL--WEAKEAPAD 116

DB 363 PEAQPEGDIAVEALEELEEPQAPAE 388

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Job time : 14.1118 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:33:53 ; Search time 16.472 Seconds
(without alignments)
587.240 Million cell updates/sec

Title: US-09-718-803A-2
Perfect score: 611
Sequence: 1 MPSGTCVCSLLGLMLDL.....LGKFLQDILWEAKEAPADK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611	100.0	117	2	US-09-046-479-2
2	611	100.0	117	2	US-08-822-897C-2
3	611	100.0	117	2	US-09-608-810A-4
4	611	100.0	117	2	US-09-404-417A-2
5	611	100.0	117	2	US-09-794-987-2
6	611	100.0	117	2	US-09-853-253-2
7	611	100.0	117	2	US-09-991-181-268
8	611	100.0	117	2	US-09-990-444-268
9	611	100.0	117	2	US-09-796-158-2
10	611	100.0	117	2	US-09-997-333-268
11	611	100.0	117	2	US-09-992-598-268
12	145	23.7	28	2	US-09-880-498-1
13	130	21.3	25	2	US-09-853-253-9
14	126	20.6	24	2	US-09-853-253-4
15	125	20.5	24	2	US-09-853-253-10
16	121	19.8	23	2	US-09-853-253-5
17	121	19.8	23	2	US-09-853-253-6
18	119	19.5	23	2	US-09-853-253-11
19	91	14.9	18	2	US-09-404-417A-11
20	90	14.7	17	2	US-09-853-253-14
21	86	14.1	119	2	US-09-046-479-4
22	86	14.1	119	2	US-08-822-897C-4
23	86	14.1	119	2	US-09-608-810A-5
24	86	14.1	119	2	US-09-404-417A-4
25	86	14.1	119	2	US-09-794-987-4
26	86	14.1	119	2	US-09-796-158-4
27	85	13.9	16	2	US-09-853-253-15

28	85	13.9	16	2	US-09-853-253-16	Sequence 16, Appl
29	79	12.9	15	2	US-09-853-253-17	Sequence 17, Appl
30	76	12.4	15	2	US-09-853-253-25	Sequence 25, Appl
31	76	12.4	352	2	US-09-902-540-10277	Sequence 10277, A
32	73	11.9	323	2	US-08-023-213B-25	Sequence 25, Appl
33	72.5	11.9	244	1	US-08-696-827-1	Sequence 1, Appl
34	72.5	11.9	773	2	US-09-252-991A-23192	Sequence 23192, A
35	71.5	11.7	589	2	US-09-134-000C-5710	Sequence 5710, Ap
36	71	11.6	556	2	US-09-524-101D-22	Sequence 22, Appl
37	70	11.5	220	1	US-08-761-248B-4	Sequence 4, Appl
38	70	11.5	255	2	US-09-949-016-10591	Sequence 10591, A
39	69.5	11.4	247	2	US-09-252-991A-27419	Sequence 27419, A
40	69.5	11.4	341	2	US-09-252-991A-27327	Sequence 27327, A
41	69.5	11.4	667	2	US-09-902-540-15196	Sequence 15196, A
42	69	11.3	406	2	US-09-252-991A-28102	Sequence 28102, A
43	69	11.3	1088	2	US-09-130-242-2	Sequence 2, Appl
44	69	11.3	1088	2	US-09-583-610D-2	Sequence 2, Appl
45	69	11.3	1088	2	US-09-949-016-6935	Sequence 6935, Ap

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

different invertebrate

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QY 1 MSPGTVCSLLLLGMLWLDLWLAGSSFLSPHQRVQORKEKPKPAKLOPRALAGWLRLPE 60
Db 1 MSPGTVCSLLLLGMLWLDLWLAGSSFLSPHQRVQORKEKPKPAKLOPRALAGWLRLPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117

RESULT 2
US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-897C-2

Query Match 100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPGTVCSLLLLGMLWLDLWLAGSSFLSPHQRVQORKEKPKPAKLOPRALAGWLRLPE 60
Db 1 MSPGTVCSLLLLGMLWLDLWLAGSSFLSPHQRVQORKEKPKPAKLOPRALAGWLRLPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
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RESULT 3
US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
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; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)....(23)
US-09-608-810A-4

Query Match 100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPGTVCSLLLLGMLWLDLWLAGSSFLSPHQRVQORKEKPKPAKLOPRALAGWLRLPE 60
Db 1 MSPGTVCSLLLLGMLWLDLWLAGSSFLSPHQRVQORKEKPKPAKLOPRALAGWLRLPE 60
QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
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RESULT 4
US-09-404-417A-2
; Sequence 2, Application US/09404417A
; Patent No. 6827729
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: TML PEPTIDES
; FILE REFERENCE: 97-04C1
; CURRENT APPLICATION NUMBER: US/09/404,417A
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-417A-2

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Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADK 117
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RESULT 5
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. 6838438
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
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; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawielak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

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Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MPSPTVCSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60
Qy 61 DGGQAEAGAELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAEAGAELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 6
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. 6897286
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2
Query Match 100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPSPTVCSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60
Db 1 MPSPTVCSLLLLGMLDLAMAGSSFLSPHQVQQRKESKPPAKLPALAGWLRPE 60
Qy 61 DGGQAEAGAELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAEAGAELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 7
US-09-991-181-268
; Sequence 268, Application US/09991181
; Patent No. 6913419
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02


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Query Match      100.0%; Score 611; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.9e-67;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSPTVCSLLLLGMLWLDLWAGSSFLSPHORVQORQKSKPKPKLQPRALAGWLRLPE 60
   |||||
DB 1 MPSPTVCSLLLLGMLWLDLWAGSSFLSPHORVQORQKSKPKPKLQPRALAGWLRLPE 60
   |||||

QY 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
   |||||
DB 61 DGGQAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
   |||||

RESULT 8
US-09-990-444-268
; Sequence 268, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
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; Sequence 268, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23

QY	DB	Sequence	Score	DB 2	Length	Indels	Gaps	0;
QY	1	MPSPGTVCSLLLLGMLWLDLWLAGSSFLSPHQRVQQRKESKKPPAKLPFRALAGWLRLPE	60					
Db	1	MPSPGTVCSLLLLGMLWLDLWLAGSSFLSPHQRVQQRKESKKPPAKLPFRALAGWLRLPE	60					
QY	61	DGQGAEGAEDLEVRFNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEAKEAPADK	117					
Db	61	DGQGAEGAEDLEVRFNAPFDVGIKLSGVQYQHSQALGKFLQDILWEEAKEAPADK	117					

Query Match 100.0%; Score 611; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.9e-67;

Mismatches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

US-09-992-598-268

/ Sequence 268, Application US/09992598

/ Patent No. 6956108

/ GENERAL INFORMATION:

; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 611; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 6.9e-67;

Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSFGTVCSSLILGLMLDLAMAGSSFLSPSEHORVQQRKSKPPAKLQPRALAGWL RPE 60

Db 1 MPSFGTVCSSLILGLMLDLAMAGSSFLSPSEHORVQQRKSKPPAKLQPRALAGWL RPE 60

Qy 61 DGGQAGAEDELEVRFNAPFDVGKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117

Db 61 DGGQAGAEDELEVRFNAPFDVGKLSGVQYQHSQALGKFLQDILWEEAKEAPADK 117

RESULT 12

US-09-880-498-1

; Sequence 1, Application US/09880498

; Patent No. 6861409

; GENERAL INFORMATION:

; APPLICANT: Zentaris AG

; TITLE OF INVENTION: Growth Hormone Secretagogues

; FILE REFERENCE: 87264-100

1 ; CURRENT APPLICATION NUMBER: US/09/880,498
2 ; CURRENT FILING DATE: 2001-06-13
3 ; PRIOR APPLICATION NUMBER: US Provisional Appln No. 6861409 60/234,928
4 ; FILING DATE: 2000-09-26
5 ; PRIOR APPLICATION NUMBER: US Provisional Appln No. 6861409 60/211,326
6 ; FILING DATE: 2000-06-13
7 ; NUMBER OF SEQ ID NOS: 1
8 ; SOFTWARE: Patentin version 3.1
9 ; SEQ ID NO 1
10 ; LENGTH: 28
11 ; TYPE: PRT
12 ; ORGANISM: rat
13 ; FEATURE:
14 ; NAME/KEY: MOD.RES
15 ; LOCATION: (3)..(3)
16 ; OTHER INFORMATION: o-n-octanoyl
17 US-09-880-498-1

Query Match 23.7%; Score 145; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GSSFLSPHEHQVQQRKESKPKPKLQPR 51
Db 1 GSSFLSPHEHQVQQRKESKPKPKLQPR 28

RESULT 13
US-09-853-253-9
; Sequence 9, Application US/09853253
; Patent No. 6897286
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-9

Query Match 21.3%; Score 130; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.2e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 FNAPFDVGKLSGVQYQQHSQALGK 100
Db 1 FNAPFDVGKLSGVQYQQHSQALGK 25

RESULT 14
US-09-853-253-4
; Sequence 4, Application US/09853253
; Patent No. 6897286
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300

Query Match 20.6%; Score 126; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 ALAGWLRPEDGGQAGAEDELEVR 75
Db 1 ALAGWLRPEDGGQAGAEDELEVR 24

RESULT 15
US-09-853-253-10
; Sequence 10, Application US/09853253
; Patent No. 6897286
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-10

Query Match 20.5%; Score 125; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 FNAPFDVGKLSGVQYQQHSQALG 99
Db 1 FNAPFDVGKLSGVQYQQHSQALG 24

Search completed: April 10, 2006, 17:35:42
Job time : 17.472 secs

not relevant

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:24:12 ; Search time 70.4907 Seconds
(without alignments)
1171.032 Million cell updates/sec

Title: US-09-718-803A-2
Perfect score: 611
Sequence: 1 MPSPGTVCSSLLGLGLMLDL.....LGKFLQDILMEAKEAPADK 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	611	100.0	117	1	GHRL_HUMAN
2	591	96.7	117	2	Q6UDE7 MACMU
3	524	85.8	117	1	GHRL_MOUSE
4	518	84.8	117	1	GHRL_RAT
5	515	84.3	117	2	Q8CHF3 MERUN
6	511	83.6	117	1	GHRL_FELCA
7	476	77.9	117	1	GHRL_CANPA
8	472.5	77.3	118	1	GHRL_PIG
9	436.5	71.4	116	1	GHRL_CAPHI
10	422.5	69.1	116	2	Q863T0 SHEEP
11	417.5	68.3	116	1	GHRL_BOVIN
12	392	64.2	91	2	Q86YF8 HUMAN
13	370.5	60.6	97	2	Q863C6 SHEEP
14	325.5	53.3	78	2	Q7TSD1 MOUSE
15	320	52.4	86	2	Q811T4 MOUSE
16	289.5	47.4	74	2	Q87B85 PIG
17	260	42.6	124	2	Q8F4B3 TRASC
18	249.5	40.8	116	2	Q8VMU7 PAVES
19	247.5	40.5	65	2	Q8TGF0 PIG
20	245.5	40.2	116	2	Q8VMU6 ANAPL
21	243.5	39.9	116	2	Q8VMU5 DRONO
22	232.5	38.1	116	2	Q7T1B9 MELGA
23	229.5	37.6	116	2	Q7T2V1 CHICK
24	229.5	37.6	116	2	Q8AV73 CHICK
25	211	34.5	114	2	Q8F4B4 TRASC
26	196.5	32.2	54	2	Q8SLF6 CEREL
27	195.5	32.0	54	2	Q8SLF2 ODOHE
28	195.5	32.0	54	2	Q8SLF8 RANTA
29	194.5	31.8	54	2	Q8SLG1 CAPHI
30	192.5	31.5	54	2	Q8SLF4 SCETA
31	190.5	31.2	52	2	Q8SLF9 SCETA

32 187 30.6 36 2 Q5Y392 HUMAN Q5Y392 homo sapien
33 180.5 29.5 54 2 Q6SLG3 SHEEP Q6SLG3 ovis aries
34 180.5 29.5 54 2 Q6SPC2 BISBI Q6SPC2 bison bison
35 178.5 29.2 54 2 Q6SLG5 KGBR Q6SLG5 kogia brevi
36 178.5 29.2 54 2 Q6SLG7 BOVIN Q6SLG7 bos taurus
37 163 26.7 40 2 Q6TGE9 PIG Q6TGE9 sus scrofa
38 146 23.9 111 1 GHRL_ONGJA Q8JFY4 anguilla ja
39 124 20.3 111 1 GHRL_ONCMY Q761Q4 oncorhynchu
40 117.5 19.2 108 2 Q4LET9 ICTPU Q4LET9 ictalurus p
41 116.5 19.1 108 2 Q4LET8 ICTPU Q4LET8 ictalurus p
42 112.5 18.4 35 2 Q6SPC3 ANAM Q6SPC3 antilocapra
43 111 18.2 32 2 Q6SLF5 CEREL Q6SLF5 cervus elap
44 110.5 18.1 107 2 Q4L142 ACASC Q4L142 acanthopagr
45 102 16.7 29 2 Q6SLG2 SHEEP Q6SLG2 ovis aries

ALIGNMENTS

RESULT 1
GHRL_HUMAN
ID GHRL_HUMAN STANDARD; PRT; 117 AA.
AC Q9UBU3; Q8TAT9; Q9H3R3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein) (Contains: Ghrelin-27; Ghrelin-28 (Ghrelin)).
DE Name=GHRL; Synonyms=MTLRP; ORFNames=UN0524/PRO1066;
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND ACYLATION OF SER-26.
RC TISSUE=Stomach;
RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
RL Nature 402:656-660(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 24-33.
RC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Wajnrajch M.P., Ten I.S., Gertner J.M., Leibell R.L.;
RT "Genomic organization of the human Ghrelin gene.";
RL J. Endocr. Genet. 1:231-233(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), TISSUE SPECIFICITY, ACYLATION OF SER-26, AND MASS SPECTROMETRY.
RC TISSUE=Stomach;
RX PubMed=12414809; DOI=10.1074/jbc.M205366200;
RA Hosoda H., Kojima M., Mizushima T., Shimizu S., Kangawa K.;
RT "Structural divergence of human ghrelin. Identification of multiple ghrelin-derived molecules produced by post-translational processing.";
RL J. Biol. Chem. 278:64-70(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wiewand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RL [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [7]
RP PROTEIN SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RL [8]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9UBU3-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
CC -!- TISSUE SPECIFICITY: Highest level in stomach. All forms are found
CC in serum as well. Other tissues compensate for the loss of ghrelin
CC synthesis in the stomach following gastrectomy.
CC -!- PTM: O-n-octanoylation is essential for activity. The O-n-
CC decanoylated forms Ghrelin-27-C10 and Ghrelin-28-C10 differ in the
CC length of the carbon backbone of the carboxylic acid bound to Ser-
CC 26. A small fraction of ghrelin, ghrelin-28-C10:1, may be modified
CC with an unsaturated carboxylic acid.
CC -!- MASS SPECTROMETRY: MW=3398.9; MW ERR=0.3; METHOD=Electrospray;
CC RANGE=24-51 (Ghrelin-28-C10); NOTE=O-decanoylated form (Ref.4).
CC -!- MASS SPECTROMETRY: MW=3397.2; MW ERR=0.5; METHOD=Electrospray;
CC RANGE=24-51 (Ghrelin-28-C10:1); NOTE=O-decanoylated form (Ref.4).
CC -!- MASS SPECTROMETRY: MW=3371.3; MW ERR=0.1; METHOD=Electrospray;
CC RANGE=24-51 (Ghrelin-28); NOTE=O-octanoylated form (Ref.4).

CC -!- MASS SPECTROMETRY: MW=3243.6; MW ERR=0.4; METHOD=Electrospray;
CC RANGE=24-50 (Ghrelin-27-C10); NOTE=O-decanoylated form (Ref.4).
CC -!- MASS SPECTROMETRY: MW=3214.6; MW ERR=0.6; METHOD=Electrospray;
CC RANGE=24-50 (Ghrelin-27); NOTE=O-octanoylated form (Ref.4).
CC -!- SIMILARITY: Belongs to the motilin family.
CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/GhrelinID327.html".
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB029434; BAA89371.1; -; mRNA.
CC EMBL; AJ252278; CAB65733.1; -; mRNA.
CC EMBL; AF296558; AAG10300.1; -; Genomic_DNA.
CC EMBL; AB035700; BAB19045.1; -; mRNA.
CC EMBL; AY359053; AAO89412.1; -; mRNA.
CC EMBL; BC025791; AAH25791.1; -; mRNA.
CC PIR; A59316; A59316.
CC PDB; IPTX; Model; A=1-117.
CC Ensembl; ENSG00000157017; Homo sapiens.
CC H-InvDB; HIX0003050; -.
CC MIM; 605353; -.
CC GO; GO:0005615; C:extracellular space; ISS.
CC GO; GO:001664; F:G-protein-coupled receptor binding; ISS.
CC GO; GO:0016608; F:growth hormone-releasing hormone activity; ISS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; ISS.
CC GO; GO:0050791; P:regulation of physiological process; ISS.
CC InterPro; IPR006737; motilin_assoc.
CC InterPro; IPR006738; motilin_ghrelin.
CC InterPro; IPR005441; Preproghrelin.
CC PANTHER; PTHR14122; Preproghrelin; 1.
CC Pfam; PF04643; Motilin_assoc; 1.
CC Pfam; PF04644; Motilin_ghrelin; 1.
CC PRINTS; PR01624; GHRELIN.
CC ProDom; PD332162; Preproghrelin; 1.
CC 3D-structure; Alternative splicing; Direct protein sequencing;
CC Hormone; Lipoprotein; Signal.
FT SIGNAL 1 23
FT PEPTIDE 24 51 Ghrelin-28.
FT PEPTIDE 24 50 Ghrelin-27.
FT PROPEP 52 117 Removed in mature form.
FT LIPID 26 26 O-decanoyl serine (in form ghrelin-27-C10
FT and form ghrelin-28-C10).
FT LIPID 26 26 O-octanoyl serine (in form ghrelin-27 and
FT form ghrelin-28).
FT VARSPLIC 37 37 Missing (in isoform 2).
FT CONFLICT 72 72 /FTID=VSP_003245.
FT SEQUENCE 117 AA; 12911 MW; 39C0572EBECA2755 CRC64;
Query Match 100.0%; Score 611; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPGTVCSSLLLLGMLWLDLWAGSSFLSPHQVQQRKESKKPPAKLPALAGWLPRPE 60
Db 1 MSPGTVCSSLLLLGMLWLDLWAGSSFLSPHQVQQRKESKKPPAKLPALAGWLPRPE 60
QY 61 DGGQAGAEDELEVRFNAPFDVGILSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
Db 61 DGGQAGAEDELEVRFNAPFDVGILSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
RESULT 2
Q6UDE7 MACMU PRELIMINARY; PRT; 117 AA.
AC Q6UDE7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)


```
CC      -!- SIMILARITY: Belongs to the motilin family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AJ243503; CAB46500.1; -; mRNA.
CC      EMBL; AB035701; BAB19046.1; -; mRNA.
CC      EMBL; AB060078; BAB69857.1; -; Genomic_DNA.
CC      EMBL; AK008658; BAB25814.1; -; mRNA.
CC      EMBL; AK008860; BAB25934.1; -; mRNA.
CC      Ensembl; ENSMUSG0000064177; Mus musculus.
CC      MGI; MGI:1930008; Ghrl.
CC      GO; GO:0005737; C:cytoplasm; IDA.
CC      GO; GO:0005615; C:extracellular space; TAS.
CC      GO; GO:0005179; F:hormone activity; TAS.
CC      InterPro; IPR006737; motilin_assoc.
CC      InterPro; IPR006738; motilin_ghrelin.
CC      InterPro; IPR005441; Preproghrelin.
CC      PANTHER; PFHR14122; Preproghrelin; 1.
CC      Pfam; PF04643; Motilin_assoc; 1.
CC      Pfam; PF04644; Motilin_ghrelin; 1.
CC      PRINTS; PR01624; GHRELIN.
CC      ProDom; PD32162; Preproghrelin; 1.
KW      Alternative splicing; Direct protein sequencing; Hormone; Lipoprotein;
KW      Signal.
FT      SIGNAL          1      23
FT      PEPTIDE        24      51
FT      PROPEP        52     117
FT      LIPID          26      26
FT      LIPID          26      26
FT      VARSPLIC       37
FT      VARSPLIC       37      Missing (in isoform 2).
FT      VARSPLIC       37      /FTID=VSP_003246.
SQ      SEQUENCE       117 AA; 13207 MW; EACE49D2E3CA7203 CRC64;

Query Match      85.8%; Score 524; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 8.9e-45;
Matches 98; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY      1  MPSPTVCSLLLGLMLDLAMAGSFLSPHEHQVQQRKESKKPAKLQPRALAGWLKPE 60
DB      1  MLSSGTICSLLLMLMDMAMAGSFLSPHEHQKQQRKESKKPAKLQPRALAGWLKPE 60

QY      61  DGGQAGAELEVRFPFDVGVIGKLSGVQYQHSQALGKFLQDILWEEKEAPADK 117
DB      61  DRGQAEETEELIRFPNPFVGVIGKLSGNAQYQHGKFLQDILWEEVKEAPADK 117

RESULT 4
GRLN_RAT
ID_GRLN_RAT      STANDARD;      PRT;      117 AA.
AC      Q9QYH7; Q9ET69;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE      releasing peptide) (Motilin-related peptide).
GN      Name=Ghrl;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridea; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), PROTEIN SEQUENCE OF 24-51,
RP      MASS SPECTROMETRY, AND ACYLATION OF SER-26.
RC      STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX      MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
RA      Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
```

```
RT      "Ghrelin is a growth-hormone-releasing acylated peptide from
RT      stomach.";
RL      Nature 402:656-660(1999).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE OF
RP      24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
RC      STRAIN=Sprague-Dawley; TISSUE=Stomach;
RX      MEDLINE=20357315; PubMed=10801861; DOI=10.1074/jbc.M002784200;
RA      Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT      "Purification and characterization of rat des-Gln14-ghrelin, a second
RT      endogenous ligand for the growth hormone secretagogue receptor.";
RL      J. Biol. Chem. 275:21995-22000(2000).
RN      [3]
RP      CHARACTERIZATION.
RX      MEDLINE=21092536; PubMed=11162448; DOI=10.1006/bbrc.2000.4039;
RA      Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT      "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
RT      in gastrointestinal tissue.";
RN      Biochem. Biophys. Res. Commun. 279:909-913(2000).
RN      [4]
RP      STRUCTURE-ACTIVITY RELATIONSHIP.
RX      MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553;
RA      Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
RA      Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
RT      "Structure-activity relationship of ghrelin: pharmacological study of
RT      ghrelin peptides.";
RL      Biochem. Biophys. Res. Commun. 287:142-146(2001).
RN      [5]
RP      REVIEW.
RX      MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA      Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT      "Ghrelin: discovery of the natural endogenous ligand for the growth
RT      hormone secretagogue receptor.";
RL      Trends Endocrinol. Metab. 12:118-122(2001).
CC      -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC      receptor type 1 (GHSR) inducing the release of growth hormone from
CC      the pituitary. Has an appetite-stimulating effect, induces
CC      adiposity and stimulates gastric acid secretion. Involved in
CC      growth regulation.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1; Synonyms=Ghrelin;
CC      IsoId=Q9QYH7-1; Sequence=Displayed;
CC      Name=2; Synonyms=del-Gln14-ghrelin;
CC      IsoId=Q9QYH7-2; Sequence=VSP_003248;
CC      -!- TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC      the stomach. Very low levels are detected in the hypothalamus,
CC      heart, lung, pancreas, intestine and adipose tissue.
CC      -!- PTM: O-n-octanoylation is essential for activity. The replacement
CC      of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC      -!- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray;
CC      RANGE=24-51 (Q9QYH7-1); NOTE=Ref.1.
CC      -!- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray;
CC      RANGE=24-50 (Q9QYH7-2); NOTE=Ref.2.
CC      -!- SIMILARITY: Belongs to the motilin family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AB029433; BAA89370.1; -; mRNA.
CC      EMBL; AB035699; BAB11956.1; -; mRNA.
CC      PIR; B59316; B59316.
CC      Ensembl; ENSRNOG0000010349; Rattus norvegicus.
CC      RGD; 632283; Ghrl.
CC      GO; GO:0005615; C:extracellular space; IC.
CC      GO; GO:0001664; F:G-protein-coupled receptor binding; IPI.
CC      GO; GO:0016608; F:growth hormone-releasing hormone activity; IDA.
CC      GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IDA.
CC      GO; GO:0050791; P:regulation of physiological process; NAS.
```

DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Alternative splicing; Direct protein sequencing; Hormone; Lipoprotein; Signal.
 FT SIGNAL 1 23 Ghrelin.
 FT PEPTIDE 24 51 Removed in mature form.
 FT PROPEP 52 117 O-octanoyl serine.
 FT LIPID 26 37 Missing (in isoform 2).
 FT VARSPPLIC 37 /FTID=VSP_003248.
 FT SEQUENCE 117 AA; 13176 MW; 8957546FE51A7691 CRC64;
 Query Match 84.8%; Score 518; DB 1; Length 117;
 Best Local Similarity 82.9%; Pred. No. 3.6e-44;
 Matches 97; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MPSFGTVCSSLLLLGLMGLDLAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPE 60
 Db 1 MVSSATICSLLLLGLMGLDLAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPE 60
 QY 61 DGGQAEAEDELEVRFNAPFDVGIKLSGVQYQHQSHQALGKFLQDILWEEAKEAPADK 117
 Db 61 DRGQAEAEDELEVRFNAPFDVGIKLSGVQYQHQSHQALGKFLQDILWEEAKEAPADK 117
 RESULT 5
 Q8CH53 MERUN
 ID Q8CH53 MERUN PRELIMINARY; PRT; 117 AA.
 AC Q8CH53;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ghrelin preproprotein.
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Gerbillinae; Meriones.
 OC NCBI_TaxID=10047;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14724148; DOI=10.1136/gut.2003.021568;
 RA Suzuki H., Masaoaka T., Hosoda H., Ota T., Minegishi Y., Nomura S.,
 RT "Helicobacter pylori infection modifies gastric and plasma ghrelin
 dynamics in Mongolian gerbils.";
 RL Gut 53:187-194(2004).
 DR EMBL; AF442491; AAC06965.1; -; mRNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0016608; F:regulation of hormone-releasing hormone activity; IEA.
 DR GO; GO:0050791; P:regulation of physiological process; IEA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
 Query Match 84.3%; Score 515; DB 2; Length 117;
 Best Local Similarity 82.1%; Pred. No. 7.2e-44;
 Matches 96; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MPSFGTVCSSLLLLGLMGLDLAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPE 60
 Db 1 MMSSGTICSLLLGLVLMVMDVAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPD 60

QY 61 DGGQAEAEDELEVRFNAPFDVGIKLSGVQYQHQSHQALGKFLQDILWEEAKEAPADK 117
 Db 61 GRGQAEAEDELEVRFNAPFDVGIKLSGVQYQHQSHQALGKFLQDILWEEAKEATDK 117
 RESULT 6
 GHRL FELCA
 ID GHRL FELCA STANDARD; PRT; 117 AA.
 AC Q6BEG6; Q6BEG5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 releasing peptide) (Motilin-related peptide).
 GN Name=GHRL;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felinae; Felis.
 OC NCBI_TaxID=9685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RC TISSUE=Stomach;
 RA Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
 RT "cDNA cloning of feline and caprine ghrelin.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Specific ligand for the growth hormone secretagogue
 receptor type 1 (GHSR) inducing the release of growth hormone from
 the pituitary. Has an appetite-stimulating effect, induces
 adiposity and stimulates gastric acid secretion. Involved in
 growth regulation (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q6BEG6-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q6BEG6-2; Sequence=VSP_011626;
 CC -1- PTM: O-octanoylation is essential for activity (By similarity).
 CC -1- SIMILARITY: Belongs to the motilin family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 DR EMBL; AB089201; BAD34670.1; -; mRNA.
 DR EMBL; AB089202; BAD34671.1; -; mRNA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Alternative splicing; Hormone; Lipoprotein; Signal.
 FT SIGNAL 1 23 By similarity.
 FT PEPTIDE 24 51 Ghrelin (By similarity).
 FT PROPEP 52 117 Removed in mature form (By similarity).
 FT LIPID 26 26 O-octanoyl serine (By similarity).
 FT VARSPPLIC 37 Missing (in isoform 2).
 FT /FTID=VSP_011626.
 SQ SEQUENCE 117 AA; 12956 MW; 8235A51447FF530 CRC64;
 Query Match 83.6%; Score 511; DB 1; Length 117;
 Best Local Similarity 82.9%; Pred. No. 1.8e-43;
 Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MPSFGTVCSSLLLLGLMGLDLAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPE 60
 Db 1 MMSSGTICSLLLGLVLMVMDVAMAGSSFLSPFHQRVQORKESSKPPAKLOPRALAGWLRLPD 60

Db 1 MPSPTVCSSLLLSFMSLWADLAMAGSSFLSPHVKQQRKESKPPAKLPQRALEGLIHP6 60
 QY 61 DGGQAEAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 Db 61 DTSQVEAGAEDELEIRNAPFDVGIKLSGAQYHQHQAQHGKFLQDVLWEEADEVLAD6 117

RESULT 7

GHR_L CANFA STANDARD; PRT; 117 AA.
 AC Q9BEF8; Q9BEF7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
 DE Name=GHLR; Synonyms=MTLRP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RC TISSUE=Gastric fundus;
 RA Tonasetto C., Wendling C., Rio M.-C., Poitras P.;
 RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog fundus.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RC TISSUE=Stomach;
 RA Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;
 RT "Dog ghrelin.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9BEF8-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9BEF8-2; Sequence=VSP 003244;
 CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -!- SIMILARITY: Belongs to the motilin family.

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 DR EMBL; AJ298295; CAC29155.1; -; mRNA.
 DR EMBL; AJ298296; CAC29156.1; -; mRNA.
 DR EMBL; AB060700; BAC75928.1; -; mRNA.
 DR Ensembl; ENSCAFG0000005129; Canis familiaris.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrel.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrel; 1.
 DR PRINTS; PR01624; GHRELIN
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Alternative splicing; Hormone; Lipoprotein; Signal.
 FT SIGNAL 1 23 By similarity.
 FT PEPTIDE 24 51 Ghrelin (By similarity).
 FT PROPEP 52 117 Removed in mature form (By similarity).
 FT LIPID 26 26 O-octanoyl serine (By similarity).

FT VARSPLIC 37 37 Missing (in isoform 2).
 FT SEQUENCE 117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;
 SQ Query Match 77.9%; Score 476; DB 1; Length 117;
 Best Local Similarity 77.8%; Pred. No. 6.1e-40;
 Matches 91; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MPSPTVCSSLLLSLGLWDLAMAGSSFLSPHVKQQRKESKPPAKLPQRALEGLIHP6 60
 Db 1 MPSLGTMCSSLLLSFVSLWYDLAMAGSSFLSPHVKQQRKESKPPAKLPQRALEGLIHP6 60
 QY 61 DGGQAEAGAEDELEVRNAPFDVGIKLSGVQVQOHSQALGKFLQDILWEEAKEAPADK 117
 Db 61 DTSQVEAGAEDELEIRNAPFDVGIKLSGAQYHQHQAQHGKFLQDVLWEEADEVLAD6 117
 RESULT 8
 GHR_L PIG STANDARD; PRT; 118 AA.
 AC Q9GKY5; Q9BDG8; Q9GKY4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
 DE Name=GHLR;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RA Kojima M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RC TISSUE=Stomach;
 RA Rousselle J., Lacroix D., Dubreuil P.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9GKY5-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9GKY5-2; Sequence=VSP 003247;
 CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -!- SIMILARITY: Belongs to the motilin family.

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 DR EMBL; AB035703; BAB19048.1; -; mRNA.
 DR EMBL; AB035704; BAB19049.1; -; mRNA.
 DR EMBL; AF308930; AAK19243.1; -; mRNA.
 DR EMBL; AY028942; AAK30002.1; -; mRNA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrel.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrel; 1.
 DR PRINTS; PR01624; GHRELIN.

DR ProDom; PD332162; Preproghrelin; 1.
 KW SIGNAL 1 24 By similarity; Signal.
 FT PEPTIDE 25 52 Ghrelin.
 FT PROPEP 53 118 Removed in mature form (By similarity).
 FT LIPID 27 27 O-octanoyl serine (By similarity).
 FT VARSPLIC 38 38 Missing (in isoform 2).
 FT CONFLICT 17 17 /FTID=VSP_003247.
 FT CONFLICT 72 72 L -> P (in Ref. 2; AAK30002).
 FT CONFLICT 72 72 K -> E (in Ref. 2; AAK30002).
 SQ SEQUENCE 118 AA; 12786 MW; 856D3E1D6DABIA76 CRC64;
 Query Match 77.3%; Score 472.5; DB 1; Length 118;
 Best Local Similarity 78.0%; Pred. No. 1.4e-39;
 Matches 92; Conservative 8; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MPSPTGTCSSLLLLGMLWLDLWAGSSFLSPHQRVQQRKSKPKKPAKLQPRALAGWLRP 59
 DB 1 MPSTGTCSSLLLSVLLWADLAMAGSSFLSPHQVKVQQRKSKPKKPAKLKPRALAGWLRP 60
 QY 60 EDGQAEAGDELEVRFNAPFDVGKLSGVQVQHSQALGKFLQDILWEEAKEAPADK 117
 DB 61 EDSGEVEGTKEIRFNAPCDVGKLSGAQSDHQGPLGKFLQDILWEEVTEAPADK 118
 RESULT 9
 GHRL_CAPHI STANDARD; PRT; 116 AA.
 ID GHRL_CAPHI Q6BEG7;
 AC Q6BEG7;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide).
 GN Name=GHRL;
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Stomach;
 RA Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
 RT "cDNA cloning of feline and caprine ghrelin.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -!- SIMILARITY: Belongs to the motilin family.
 CC -----
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 CC -----
 CC EMBL; AB089200; BAD34669.1; -; mRNA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Hormone; Lipoprotein; Signal.
 KW SIGNAL 1 23 By similarity.
 FT PEPTIDE 24 50 Ghrelin (By similarity).
 FT

FT PROPEP 51 116 Removed in mature form (By similarity).
 FT LIPID 26 26 O-octanoyl serine (By similarity).
 SQ SEQUENCE 116 AA; 12935 MW; CDA67971D72E3303 CRC64;
 Query Match 71.4%; Score 436.5; DB 1; Length 116;
 Best Local Similarity 71.8%; Pred. No. 5.7e-36;
 Matches 84; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
 QY 1 MPSPTGTCSSLLLLGMLWLDLWAGSSFLSPHQRVQQRKSKPKKPAKLQPRALAGWLRP 60
 DB 1 MPARTTICSSLLLSLWMDLAMAGSSFLSPHQKL-QRKEPKKSGRLKPRALAGWLRP 59
 QY 61 DGGQAEAGDELEVRFNAPFDVGKLSGVQVQHSQALGKFLQDILWEEAKEAPADK 117
 DB 60 VGSQEGAEDELEIRFNAPFNIGIKLSGAQSLQHGQTLGKFLQDILWEEAETLADE 116
 RESULT 10
 Q863LO SHEEP PRELIMINARY; PRT; 116 AA.
 ID Q863LO SHEEP Q863LO;
 AC Q863LO;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Preproghrelin precursor.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Stomach;
 RA Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;
 RT "sheep ghrelin.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB060599; BAC75928.1; -; mRNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
 DR GO; GO:0050791; P:regulation of physiological process; IEA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 DR Signal.
 KW SIGNAL 1 23 Potential.
 FT CHAIN 24 50 ghrelin.
 SQ SEQUENCE 116 AA; 12977 MW; B78ECA3DBF0E568E CRC64;
 Query Match 59.1%; Score 422.5; DB 2; Length 116;
 Best Local Similarity 70.1%; Pred. No. 1.5e-34;
 Matches 82; Conservative 14; Mismatches 20; Indels 1; Gaps 1;
 QY 1 MPSPTGTCSSLLLLGMLWLDLWAGSSFLSPHQRVQQRKSKPKKPAKLQPRALAGWLRP 60
 DB 1 MPARTTICSSLLLSLWMDLAMAGSSFLSPHQKL-QRKEPKKSGRLKPRALAGWLRP 59
 QY 61 DGGQAEAGDELEVRFNAPFDVGKLSGVQVQHSQALGKFLQDILWEEAKEAPADK 117
 DB 60 VGSQEGAEDELEIRFNAPFNIGIKLSGAQSLQHGQTLGKFLQDILWEEAETLADE 116
 RESULT 11
 GHRL_BOVIN STANDARD; PRT; 116 AA.
 ID GHRL_BOVIN Q9BDJ6; Q9GKV6;
 AC Q9BDJ6; Q9GKV6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)

OC	Homo.
RN	[1]
RA	NUCLEOTIDE SEQUENCE.
RL	Jeffery P.L., Herington A.C., Chopin L.K.;
DR	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY184207; AAC27351.1; -, mRNA.
DR	Ensembl; ENSG00000157017; Homo sapiens.
DR	GO; GO:0005576; C:extracellular region; IEA.
DR	GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR	GO; GO:0050791; P:regulation of physiological process; IEA.
DR	InterPro; IPR006738; motilin_ghrelin.
DR	InterPro; IPR005441; Preproghrelin.
DR	PANTHER; PTHR14122; Preproghrelin; 1.
DR	Pfam; PF04644; Motilin_ghrelin; 1.
DR	PRINTS; PR01624; GHRELIN.
SQ	SEQUENCE 91 AA; 9972 MW; E7E532D32A3F8609 CRC64;
Query Match	64.2%; Score 392; DB 2; Length 91;
Best Local Similarity	96.2%; Pred. No. 1.3e-31;
Matches	76; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 MPSPGVTCVSLLLGLMLWLDLAMAGSSFLSPHQRVQORKSKPPAKIQLPRALAGWLURPE 60
Dd	1 MPSPGVTCVSLLLGLMLWLDLAMAGSSFLSPHQRVQORKSKPPAKIQLPRALAGWLURPE 60
Qy	61 DGGQAEGAEDEVRFNAP 79
Dd	61 DGGQAEGAEDEVRRPQP 79
RESULT 13	
Q863C6 SHEEP	
ID	Q863C6 SHEEP PRELIMINARY; PRT; 97 AA.
AC	Q863C6;
DT	01-JUN-2003 (TrEMBLrel_24, Created)
DT	01-JUN-2003 (TrEMBLrel_24, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel_25, Last annotation update)
DE	Ghrelin-like protein (fragment).
OS	Ghrelin aries (Sheep).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC	Pecora; Bovidae; Caprinae; Ovis.
OX	NCBI_TaxID=9944;
RN	[1]
RA	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Stomach fundis region;
RD	Ford S.P., Lang L.A.;
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AV228762; AAC47381.1; -, mRNA.
DR	GO; GO:0005576; C:extracellular region; IEA.
DR	GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR	GO; GO:0050791; P:regulation of physiological process; IEA.
DR	InterPro; IPR006737; motilin_assoc.
DR	InterPro; IPR006738; motilin_ghrelin.
DR	InterPro; IPR005441; Preproghrelin.
DR	PANTHER; PTHR14122; Preproghrelin; 1.
DR	Pfam; PF04643; Motilin_assoc; 1.
DR	Pfam; PF04644; Motilin_ghrelin; 1.
DR	PRINTS; PR01624; GHRELIN.
DR	ProDom; PD332162; Preproghrelin; 1.
FT	NON_TER 1
FT	NON_TER 97
SQ	SEQUENCE 97 AA; 10890 MW; 969622786BBD15B CRC64;
Query Match	60.6%; Score 370.5; DB 2; Length 97;
Best Local Similarity	72.4%; Pred. No. 2.1e-29;
Matches	71; Conservative 11; Mismatches 15; Indels 1; Gaps 1;
Qy	15 MLMULDAMAGSSFLSPHQRVQORKSKPPAKIQLPRALAGWLURPEDGQAGEADELEV 74
Dd	1 LLMWLDAMAGSSFLSPHQKL-QRKEFPKPSGBLKPRALEGFDPDFVGSGEAGELEI 59

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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:24:12 ; Search time 220.509 Seconds
(without alignments)
1171.032 Million cell updates/sec

Title: US-09-718-803A-5

Perfect score: 1905

Sequence: 1 MWNPBSEEGFNLTADLD.....KLSTLKDESSRAWTESSINT 366

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1905	100.0	366	1	GHSR HUMAN
2	1855	97.4	360	2	Q6B7N9_MACFA
3	1789	93.9	364	1	GHSR RAT
4	1788	93.9	364	1	GHSR MOUSE
5	1771	93.0	366	1	GHSR_PIG
6	1754	92.1	366	2	Q8MH75_SHEEP
7	1411	74.1	347	2	Q7ZT14_CHICK
8	1388	72.9	289	2	Q6ISR8_HUMAN
9	1308	68.7	331	2	Q7ZZJ9_CHICK
10	1105	58.0	385	2	Q6YQ23_ACASC
11	1079.5	56.7	374	2	Q93412_PPERC
12	1075.5	56.5	394	2	Q4STY3_TETNG
13	1010	53.0	267	2	Q7ZZJ8_CHICK
14	871	45.7	215	2	Q711Q7_CHICK
15	863.5	45.3	412	1	MTLR_HUMAN
16	862	45.2	363	2	Q93413_9PERC
17	832.5	43.7	211	2	Q711Q8_CHICK
18	809.5	42.5	295	2	Q6YQ22_ACASC
19	792	41.6	286	2	Q4RFP2_TETNG
20	696	36.5	145	2	Q97914_SHEEP
21	648.5	34.0	514	2	Q4SB84_TETNG
22	648	34.0	559	2	Q93414_9PERC
23	620	32.5	123	2	Q80UB2_MOUSE
24	569.5	29.9	117	2	Q58M10_RAT
25	494.5	26.0	327	2	Q4S774_TETNG
26	483.5	25.4	424	1	NTR1_MOUSE
27	481.5	25.3	365	2	Q4SP89_TETNG
28	478	25.1	407	2	Q58CW4_BOVIN
29	475.5	25.0	413	2	Q65YS4_BOMMO
30	471	24.7	493	2	Q7RTK4_ANOGA
31	468.5	24.6	395	2	Q8BZ39_MOUSE

32	468	24.6	422	2	Q538H7_RANCA	Q538h7 rana catesb
33	466.5	24.5	395	2	Q91276_MOUSE	Q91276 mus musculus
34	464	24.4	418	1	NTR1_HUMAN	P30989 homo sapien
35	463.5	24.3	395	2	Q9ESQ4_RAT	Q9esq4 rattus norv
36	463.5	24.3	395	2	Q9JIB1_RAT	Q9jib1 rattus norv
37	461.5	24.2	424	1	NTR1_RAT	P20789 rattus norv
38	461.5	24.2	556	1	CAPAR_DROME	Q81tc7 drosophila
39	459	24.1	346	2	Q5ICC7_HELAM	Q5icc7 helicoverpa
40	458	24.0	346	2	Q6VYH4_HELZE	Q6vyh4 heliothis z
41	454.5	23.9	426	2	Q8NE20_HUMAN	Q8ne20 homo sapien
42	452.5	23.8	403	2	Q7LDP6_HUMAN	Q7ldp6 homo sapien
43	452.5	23.8	426	2	Q9HB89_HUMAN	Q9hb89 homo sapien
44	445	23.4	415	2	Q96AMS_HUMAN	Q96ams homo sapien
45	444	23.3	412	2	Q7LCS4_HUMAN	Q7lcs4 homo sapien

RESULT 1

ID	GHSR_HUMAN	STANDARD;	PRT;	366 AA.
AC	Q92847; Q92848; Q96RJ7;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing peptide receptor) (GHRP) (Ghrelin receptor).			
DE	Name=GHSR;			
GN	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORMS 1A AND 1B).			
RC	TISSUE=Pituitary;			
RX	MEDLINE=96337798; PubMed=868086;			
RA	Howard A.D., Feighner S.D., Cully D.F., Arena J.P., Liberato P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L., Palyha O.C., Anderson J., Pares P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S., Chung L.-Y., Elbrecht A., Dashkevich M., Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G., Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;			
BT	"A receptor in pituitary and hypothalamus that functions in growth hormone release.";			
RT	Science 273:974-977(1996).			
RN	[2]			
RX	MEDLINE=21255649; PubMed=11356716; DOI=10.1210/en.142.6.2649;			
RA	Petersenn S., Rasch A.C., Penschorn M., Beil F.U., Schulte H.M.;			
RA	"Genomic structure and transcriptional regulation of the human growth hormone secretagogue receptor.";			
RT	Endocrinology 142:2649-2659(2001).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1A AND 1B).			
RA	Kopatz S.A., Aronstam R.S., Sharma S.V.;			
RT	"cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";			
RT	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	FUNCTION.			
RX	MEDLINE=21219832; PubMed=11322507; DOI=10.1385/ENDO.14.1.009;			
RA	Smith R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D., Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.;			
RT	"Growth hormone secretagogue receptor family members and ligands.";			
RT	Endocrine 14:9-14(2001).			
RN	[5]			
RP	FUNCTION.			
RX	MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;			
RA	Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;			
RT	"Ghrelin is a growth-hormone-releasing acylated peptide from			

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RT stomach. ";
RL Nature 402:656-660(1999).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1A;
CC IsoId=Q92847-1; Sequence=Displayed;
CC Name=1B;
CC IsoId=Q92847-2; Sequence=VSP_001916, VSP_001917;
CC -!- TISSUE SPECIFICITY: Pituitary and hypothalamus.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U60179; AAC50653.1; -; mRNA.
DR EMBL; U60181; AAC50654.1; -; mRNA.
DR EMBL; AF369786; AAK71539.1; -; Genomic DNA.
DR EMBL; AF369786; AAK71540.1; -; Genomic DNA.
DR EMBL; AY429112; AAR07907.1; -; mRNA.
DR EMBL; AY322544; AAP84357.1; -; Genomic DNA.
DR Ensembl; ENSG00000121853; Homo sapiens.
DR HGNC; HGNC:4267; GHSR.
DR MIM; 601898; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004930; P:G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PANTHER; PTHR19284:SP51; GHS1_receptor; 1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 40
FT Extracellular (Potential).
FT TRANSMEM 41 66
FT TOPO_DOM 67 72
FT TOPO_DOM 73 96
FT TRANSMEM 97 117
FT TOPO_DOM 118 139
FT TRANSMEM 140 162
FT TOPO_DOM 163 183
FT TRANSMEM 184 211
FT TOPO_DOM 212 235
FT TRANSMEM 236 263
FT TOPO_DOM 264 285
FT TRANSMEM 286 302
FT TOPO_DOM 303 326
FT TRANSMEM 327 366
FT CARBOHYD 13 13
FT CARBOHYD 27 27
FT DISULFID 116 198
FT VARSPIC 266 289
FT FTID=VSP_001916.
FT Missing (in isoform 1B).
FT VARSPLIC 290 366
FT FTID=VSP_001917.
FT Missing (in isoform 1B).
SQ SEQUENCE 366 AA; 41329 MW; D1B62710DA9DC0C6 CRC64;
Query Match 100.0%; Score 1905; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 366; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWNATPSEPGFNLTADLDWDASPGNDSLGDELLQLPAPLLAGVTATCTVALFVVGIAQ 60
DB 1 MWNATPSEPGFNLTADLDWDASPGNDSLGDELLQLPAPLLAGVTATCTVALFVVGIAQ 60
QY 61 NLLTMLVVSRRPRELRTTNLTNLSMAFSDLLIFLCMPDLVLRLWOYRPNWFGDLLCKLFQ 120
DB 61 NLLTMLVVSRRPRELRTTNLTNLSMAFSDLLIFLCMPDLVLRLWOYRPNWFGDLLCKLFQ 120
QY 121 FVSECTYATVLTITALSVERIFAICPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFV 180
DB 121 FVSECTYATVLTITALSVERIFAICPLRAKVVVTKGRVKLVFVIWAVAFCSAGPIFV 180
QY 191 LVGVEHENGTPDWTNECRPTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLSLIGRKLW 240
DB 191 LVGVEHENGTPDWTNECRPTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLSLIGRKLW 240
QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPFGSLIAQI 300
DB 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPFGSLIAQI 300
QY 301 SQYCNLVSVFLYLSAAINPILYNIMSKYRVAVFRLGFPFQSQRKSLTLKDESSRAWT 360
DB 301 SQYCNLVSVFLYLSAAINPILYNIMSKYRVAVFRLGFPFQSQRKSLTLKDESSRAWT 360
QY 361 ESSINT 366
DB 361 ESSINT 366
RESULT 2
Q6B7N9 MACFA PRELIMINARY; PRT; 360 AA.
AC Q6B7N9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Growth hormone secretagogue receptor (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hellings S.E. III.;
RL "Macaca fascicularis growth hormone secretagogue receptor cloning.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AY675630; AAT77421.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; P:growth hormone-releasing activity; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 360 AA; 40700 MW; DAC4AC726EE9468E CRC64;
Query Match 97.4%; Score 1855; DB 2; Length 360;
Best Local Similarity 98.9%; Pred. No. 4.3e-122;
Matches 356; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Qy 7 SEEPFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGIGNLLTML 66
 Db 1 SEEPFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGIGNLLTML 60
 Qy 67 VVSFRRLRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYPMWFGDLCKLFOFVSESC 126
 Db 61 VVSFRRLRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYPMWFGDLCKLFOFVSESC 120
 Qy 127 TYATVLTITLTSVRYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGIFVVLVGVGH 186
 Db 121 TYATVLTITLTSVRYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGIFVVLVGVGH 180
 Qy 187 ENGTPDWDTECRTEFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLWRRRGD 246
 Db 181 ENGTPDWDTECRTEFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLWRRRGD 240
 Qy 247 AVVGASLRDQNHKTQVKMLAVVFAFVILCMLPFFHVGRLYFVSKSPGSLLEIAQISQYCNL 306
 Db 241 AVVGASLRDQNHKTQVKMLAVVFAFVILCMLPFFHVGRLYFVSKSPGSLLEIAQISQYCNL 300
 Qy 307 VSFVLYLSAAILNIPILYNIMSKYRVAVFRLLGPEFSPQSKLSTLKDESSRAWTESSINT 366
 Db 301 VSFVLYLSAAILNIPILYNIMSKYRVAVFRLLGPEFSPQSKLSTLKDESSRAWTESSINT 360

RESULT 3
 GHSR RAT STANDARD; PRT; 364 AA.
 AC 008725;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing peptide receptor) (GHRP) (Ghrelin receptor).
 DE peptide receptor (GHRP) (Ghrelin receptor).
 GN Name=Ghr;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pituitary;
 RX MEDLINE=97246555; PubMed=3092793; DOI=10.1210/me.11.4.415;
 RA McKee K.K., Palyha O.C., Feighner S.D., Hreniuk D.L., Tan C.P., Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;
 RT "Molecular analysis of rat pituitary and hypothalamic growth hormone secretagogue receptors.";
 RL Mol. Endocrinol. 11:415-423(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 1-240.
 RC STRAIN=Wistar; TISSUE=Pituitary;
 RX MEDLINE=98100386; PubMed=9437732; DOI=10.1016/S0196-9781(97)00263-5;
 RA Yokote R., Sato M., Matsubara S., Onye H., Niimi M., Murao K., Takahara J.;
 RT "Molecular cloning and gene expression of growth hormone-releasing peptide receptor in rat tissues.";
 RL Peptides 19:15-20(1998).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from stomach.";
 RL Nature 402:656-660(1999).
 CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins. Stimulates growth hormone secretion. Binds also other growth hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6) as well as non-peptide, low molecular weight secretagogues (e.g. L-692,429, MK-0677, adenosine) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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 CC -----
 DR EMBL; U94321; AAC53156.1; -; mRNA.
 DR EMBL; AB001982; BAA21777.1; ALT INIT; mRNA.
 DR Ensembl; ENSRNOG0000024119; Rattus norvegicus.
 DR RGD; 621397; Ghr.
 DR GO; GO:0016021; C: integral to membrane; TAS.
 DR GO; GO:0005331; F: growth hormone receptor binding; TAS.
 DR GO; GO:0001616; F: growth hormone secretagogue receptor activity; IDA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IDA.
 DR GO; GO:0045923; P: positive regulation of fatty acid metabolism; IMP.
 DR InterPro; IPR003905; GHS1_receptor.
 DR PANTHER; PTHR19264.SFS1; GHS1_receptor; 1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01417; GHSRECEPTOR.
 DR PRINTS; PR00237; GPCRHHODOPSIN.
 DR PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS00262; G PROTEIN RECP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer; Transmembrane.
 CC
 FT TOPO_DOM 1 40 Extracellular (Potential).
 FT TRANSMEM 41 66 1 (Potential).
 FT TOPO_DOM 67 72 Cytoplasmic (Potential).
 FT TRANSMEM 73 96 2 (Potential).
 FT TOPO_DOM 97 117 Extracellular (Potential).
 FT TRANSMEM 118 139 3 (Potential).
 FT TOPO_DOM 140 162 Cytoplasmic (Potential).
 FT TRANSMEM 163 183 4 (Potential).
 FT TOPO_DOM 184 211 Extracellular (Potential).
 FT TRANSMEM 212 235 5 (Potential).
 FT TOPO_DOM 236 263 Cytoplasmic (Potential).
 FT TRANSMEM 264 285 6 (Potential).
 FT TOPO_DOM 286 302 Extracellular (Potential).
 FT TRANSMEM 303 326 7 (Potential).
 FT TOPO_DOM 327 364 Cytoplasmic (Potential).
 FT CARBOHYD 13 13 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 26 26 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 187 187 N-linked (GlcNAc. .) (Potential).
 FT DISULFID 115 197 By similarity.
 SQ SEQUENCE 364 AA; 40963 MW; DCBF559BE061EE9 CRC64;
 Query Match 93.9%; Score 1789; DB 1; Length 364;
 Best Local Similarity 95.6%; Pred. No. 1.8e-117; Indels 2; Gaps 2;
 Matches 350; Conservative 5; Mismatches 9;
 Qy 1 MNATPSEEPFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGIG 60
 Db 1 MNATPSEEPFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGIG 59
 Qy 61 NLTLMLVVSFRRLRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYPMWFGDLCKLFO 120
 Db 60 NLTLMLVVSFRRLRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYPMWFGDLCKLFO 119
 Qy 121 FVSESCYATVLTITLTSVRYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGIFV 180
 Db 120 FVSESCYATVLTITLTSVRYFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGIFV 179
 Qy 181 LVGVEHENGTPDWDTECRTEFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 240
 Db 180 LVGVEHENGTPDWDTECRTEFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 239
 Qy 241 RRRRGDAVVGASLRDQNHKTQVKMLAVVFAFVILCMLPFFHVGRLYFVSKSPGSLLEIAQI 300
 Db 240 -RRRGDAVVGASLRDQNHKTQVKMLAVVFAFVILCMLPFFHVGRLYFVSKSPGSLLEIAQI 298
 Qy 301 SQYCNLYSVFLYLSAAILNIPILYNIMSKYRVAVFRLLGPEFSPQSKLSTLKDESSRAW 360
 Db 299 SQYCNLYSVFLYLSAAILNIPILYNIMSKYRVAVFRLLGPEFSPQSKLSTLKDESSRAW 358

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QY 361 ESSINT 366
Db 359 KSSINT 364

RESULT 4
GHSR_MOUSE
ID GHSR_MOUSE STANDARD; PRT; 364 AA.
AC Q99P50; Q9BWX9; Q91282;
DT 28-FEB-2003 (Rel. 41, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=Ghsr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrester A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gusincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltsev L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenawa Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
[2]
RN NUCLEOTIDE SEQUENCE OF 1-183
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA Kacsoh B.;
RT "Cloning of mouse ghrelin/growth hormone secretagogue receptor cDNA by
RT rapid amplification of cDNA ends (RACE).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE OF 73-257.
RC STRAIN=129S3/SvimJ;
RA Peng X., Frohman L.A., Kineman R.D.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692,429, MK-0677, adenosine) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AK049671; BAC33866.1; -; mRNA.
DR EMBL; AY056474; AAL13336.1; -; mRNA.
DR EMBL; AF332997; AAG61141.1; -; mRNA.
DR Ensembl; ENSMUSG0000051136; Mus musculus.
DR MGI; MGI:2441906; Ghr.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0001616; F:growth hormone secretagogue receptor activity; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR PANTHER; PTHR19264:SF51; GHS1_receptor; 1.
DR Pfam; PF00001; 7tm.1. 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 40 Extracellular (Potential).
FT TRANSMEM 41 66 1 (Potential).
FT TOPO_DOM 67 72 Cytoplasmic (Potential).
FT TRANSMEM 73 96 2 (Potential).
FT TOPO_DOM 97 117 Extracellular (Potential).
FT TRANSMEM 118 139 3 (Potential).
FT TOPO_DOM 140 162 Cytoplasmic (Potential).
FT TRANSMEM 163 183 4 (Potential).
FT TOPO_DOM 184 211 Extracellular (Potential).
FT TRANSMEM 212 235 5 (Potential).
FT TOPO_DOM 236 263 Cytoplasmic (Potential).
FT TRANSMEM 264 285 6 (Potential).
FT TOPO_DOM 286 302 Extracellular (Potential).
FT TRANSMEM 303 326 7 (Potential).
FT TOPO_DOM 327 364 Cytoplasmic (Potential).
FT CARBOHYD 13 13 N-linked (GLCNAc. .) (Potential).
FT CARBOHYD 26 26 N-linked (GLCNAc. .) (Potential).
FT CARBOHYD 187 187 N-linked (GLCNAc. .) (Potential).
FT DISULFID 115 197 By similarity.
FT CONFLICT 59 59 G -> S (in Ref. 2).
SQ SEQUENCE 364 AA; 40969 MW; 8F1214E59EF3B2E8 CRC64;
Query Match 93.9%; Score 1788; DB 1; Length 364;
Best Local Similarity 95.4%; Pred. No. 2.2e-117;
Matches 349; Conservative 6; Mismatches 9; Indels 2; Gaps 2;
QY 1 MNATPSEEPGNVTLADLDWDASFGNDSLGDELLQLFPAPILAGVTATCVAFVWGATG 60
Db 1 MNATPSEEPGNVTLADLDWDASFGNDSLGDELLQLFPAPILAGVTATCVAFVWGATG 59
QY 61 NLLTMLVVSREPRELTTNLYLSSMAFSDLLIFLCMPDLVRLMQRPNWFGDLLCKLFQ 120
Db 60 NLLTMLVVSREPRELTTNLYLSSMAFSDLLIFLCMPDLVRLMQRPNWFGDLLCKLFQ 119
QY 121 FVSECTYATVLTITALSVERFYFAICFPLRAKVVTGKRVKLVFVIMAWAFCSAGPIFV 180
Db 120 FVSECTYATVLTITALSVERFYFAICFPLRAKVVTGKRVKLVFVIMAWAFCSAGPIFV 179
QY 181 LVGVEHNGTDPWDTNECRPTPEFAVRSGLLITVWVSSIFPFLPVFCLTVLYSLIGRLW 240
Db 180 LVGVEHNGTDPWDTNECRPTPEFAVRSGLLITVWVSSIFPFLPVFCLTVLYSLIGRLW 239
QY 241 RRRGDVAVGASLRDQNHKQVTKMLAVVVFVAFILCWLPFHVGRVLFKSPFPGSLIAQI 300
Db 240 -RRGDAAVGSRLRDQNHKQVTKMLAVVVFVAFILCWLPFHVGRVLFKSPFPGSLIAQI 298
QY 301 SQYCNLYSVFLYLSAAINPILYIMSKKYVAVFRLGPFPPFSQKSLSTLKDESSRAWT 360
Db 301 SQYCNLYSVFLYLSAAINPILYIMSKKYVAVFRLGPFPPFSQKSLSTLKDESSRAWT 360

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Db 299 SOYCNLVSVFLVYLSAAINPILYNIMSKYRVAVFKLLGFBSFSQKSLSTLKDESSRAWT 358
Qy 361 ESSINT 366
Db 359 KSSINT 364

RESULT 5
ID GHRS_PIG STANDARD; PRT; 366 AA.
AC Q95254; Q95255;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Growth hormone secretagogue receptor type 1 (GHS-R) (GH-releasing
DE peptide receptor) (GHRP) (Ghrelin receptor).
GN Name=GHSR;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1A AND 1B).
RC STRAIN=Yorkshire; TISSUE=Pituitary;
RX MEDLINE=96337998; PubMed=8688086;
RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P., Liberator P.A.,
RA Rosenblum C.I., Hamelin M., Hreniuk D.L., Paluya O.C., Anderson J.,
RA Paresse P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S.,
RA Chung L.-Y., Ebrecht A., Dashkevich M., Heavens R., Rigby M.,
RA Srinathalingji D.J.S., Dean D.C., Melillo D.G., Patchett A.A.,
RA Nargund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M.,
RA Smith R.G., van der Ploeg L.H.T.;
RT "A receptor in pituitary and hypothalamus that functions in growth
RT hormone release";
RL Science 273:974-977(1996).
CC -!- FUNCTION: Receptor for ghrelin, coupled to G-alpha-11 proteins.
CC Stimulates growth hormone secretion. Binds also other growth
CC hormone releasing peptides (GHRP) (e.g. Met-enkephalin and GHRP-6)
CC as well as non-peptide, low molecular weight secretagogues (e.g.
CC L-692, 429, MK-0677, adenosine).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1A;
CC IsoId=Q95254-1; Sequence=Displayed;
CC Name=1B;
CC IsoId=Q95254-2; Sequence=VSP_001918, VSP_001919;
CC -!- TISSUE SPECIFICITY: Pituitary and hypothalamus.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U60178; AAC48630.1; -; mRNA.
DR EMBL; U60180; AAC48631.1; -; mRNA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PANTHER; PTHR19264:SF51; GHS1_receptor; 1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 40 Extracellular (Potential).
FT TRANSMEM 41 66 1 (Potential).
FT TOPO_DOM 67 72 Cytoplasmic (Potential).
FT TRANSMEM 73 96 2 (Potential).

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FT FT TOPO_DOM 97 117 Extracellular (Potential).
FT FT TRANSMEM 118 139 3 (Potential).
FT FT TOPO_DOM 140 162 Cytoplasmic (Potential).
FT FT TRANSMEM 163 183 4 (Potential).
FT FT TOPO_DOM 184 211 Extracellular (Potential).
FT FT TRANSMEM 212 235 5 (Potential).
FT FT TOPO_DOM 236 263 Cytoplasmic (Potential).
FT FT TRANSMEM 264 285 6 (Potential).
FT FT TOPO_DOM 286 302 Extracellular (Potential).
FT FT TRANSMEM 303 326 7 (Potential).
FT FT TOPO_DOM 327 366 Cytoplasmic (Potential).
FT FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT FT CARBOHYD 27 27 N-linked (GlcNAc...) (Potential).
FT FT DISULFID 116 198 By similarity.
FT FT VARSPPLIC 266 289 AVVVFATILCWLPHPVGRYLFPSKS -> GGSQCALELSLPG
FT FT PLHSSCLFSSP (in isoform 1B).
FT FT /FTID=VSP_001918.
FT FT Missing (in isoform 1B).
FT FT /FTID=VSP_001919.
FT FT SEQUENCE 366 AA; 41195 MW; 2C850B3EF61B7C1C CRC64;
SQ SEQUENCE 366 AA; 41195 MW; 2C850B3EF61B7C1C CRC64;

Query Match 93.08; Score 1771; DB 1; Length 366;
Best Local Similarity 93.2%; Pred. No. 3.4e-116;
Matches 341; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MNWATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALFVVGIAQ 60
Db 1 MNWATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVALFVVGIAQ 60
Qy 61 NLITMLVSVRFRELTTNNLYLSMAFSDLLIFLCMPDLVRLVQYRPNWPGDILLCKLFQ 120
Db 61 NLITMLVSVRFRELTTNNLYLSMAFSDLLIFLCMPDLVRLVQYRPNWPGDILLCKLFQ 120
Qy 121 FVSESCYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFVWAVAFCSAGPIFV 180
Db 121 FVSESCYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFVWAVAFCSAGPIFV 180
Qy 181 LVGVHEHNGTDPWDTNECRTEFAVRSGLLTVMWVSSIFPFLPVFCLTVLYSLIGRKLM 240
Db 181 LVGVHEHNGTDPWDTNECRTEFAVRSGLLTVMWVSSIFPFLPVFCLTVLYSLIGRKLM 240
Qy 241 RRRRGDAVVGASLRDQNHKOTVMKLVAVVFAFVILCWLPFHVGRYLFKSFEPSGLSIAQI 300
Db 241 RRRRGDAVVGASLRDQNHKOTVMKLVAVVFAFVILCWLPFHVGRYLFKSFEPSGLSIAQI 300
Qy 301 SOYCNLVSVFLVYLSAAINPILYNIMSKYRVAVFKLLGFBSFSQKSLSTLKDESSRAWT 360
Db 301 SOYCNLVSVFLVYLSAAINPILYNIMSKYRVAVFKLLGFBSFSQKSLSTLKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366

RESULT 6
Q8MHZ5_SHEEP PRELIMINARY; PRT; 366 AA.
ID Q8MHZ5_SHEEP PRELIMINARY; PRT; 366 AA.
AC Q8MHZ5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Ghrelin/growth hormone secretagogue receptor.
DE Ovis aries (Sheep).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary gland;
RA Murata T., Ikegami R., Morita Y., Shinozaki K.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

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CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AY093949; AAM19734.1; -; mRNA.
DR EMBL; AY093950; AAM19735.1; -; mRNA.
DR EMBL; AY093948; AAM19733.1; -; mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016520; F: growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F: G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 366 AA; 41487 MW; 2F276651BC6CSD57 CRC64;

Query Match          92.1%; Score 1754; DB 2; Length 366;
Best Local Similarity 92.3%; Pred. No. 5.2e-115;
Matches 338; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 MWNATPSEPGFNLTLADLDASPGNDSLGDELLQLFPAPLAGVTATCVAFVVGIAQ 60
DB 1 MWNATRSEELGNLTLDPDWDAAFDNDSLTDLPPLPAPLAGVTATCVAFVVGIAQ 60

QY 61 NLLTMLVSVRRFELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
DB 61 NLLTMLVSVRRFELRTTNLYLSSMAFSDLLIFLCMPDLVRLWYRPNWLGDLLCKLFQ 120

QY 121 FVSECTVATVLTITALSVERFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFV 180
DB 121 FVSECTVATVLTITALSVERFAICFPLRAKVVTGKRVKLVIAIWAFAFCSAWPIFM 180

QY 181 LVGVEHENGTPDPTNECRPTFAVRSGLLTVMWVSSIFFPVFCITVLYSLIGRKLW 240
DB 181 LVGVEHENGTPDPTNECRATEFAVRSGLLTVMWVSSIFFPVFCITVLYSLIGRKLW 240

QY 241 RRRRGDAVVGASLRDQNHQTVKMLAVVVFAPILCWLPHFVGRYLFKSFPGSLEIAQI 300
DB 241 RRRSEVVVGASLRDQNHQTVKMLAVVVFAPVLCWLPHFVGRYLFKSFPGSVEIAQI 300

QY 301 SQYCNLVSEVLYFYLGAANPILYNIMSKKYRVAVFRLGFPFSPQRKSLTKDESSRAWT 360
DB 301 SQYCNLVSEVLYFYSAAINPILYNIMSKKYRVAVFRLGFPFSPQRKSLTKDESSRAWT 360

QY 361 ESSINT 366
DB 361 ESSINT 366

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RESULT 7
Q7ZT14 CHICK PRELIMINARY; PRT; 347 AA.
ID Q7ZT14;
AC Q7ZT14;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE Growth hormone secretagogue receptor type 1a.
GN Name=Ghr; Synonym=Ghsr1a;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=white leghorn; TISSUE=Kidney, and Pituitary;
RX MEDLINE=22874039; PubMed=14511992; DOI=10.1016/S0016-6480(03)00247-8;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tsushima N.,
RA Wakita M., Shimada K.;

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RT "Molecular characterization of chicken growth hormone secretagogue
RT receptor gene.";
RL Gen. Comp. Endocrinol. 134:198-202(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AB095995; BAC76444.1; -; mRNA.
DR EMBL; AB095994; BAC76443.1; -; Genomic DNA.
DR Ensembl; ENSGALG0000009187; Gallus gallus.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016520; F: growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F: G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 347 AA; 39439 MW; 7A7543A9A4222F4 CRC64;

Query Match          74.1%; Score 1411; DB 2; Length 347;
Best Local Similarity 76.5%; Pred. No. 5.4e-91;
Matches 264; Conservative 37; Mismatches 44; Indels 0; Gaps 0;

QY 22 DASPGNDSLGDELLQLFPAPLAGVTATCVAFVVGIAGNLLTMLVSVRRFELRTTNLY 81
DB 3 EGSENRTGGESPLRLFPAPVLTGTVACVLLFVVGVLGNLMTMLVSVRRFDMRTTTFY 62

QY 82 LSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQFVSECTVATVLTITALSVER 141
DB 63 LSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQFVSECTVLTILNITALSVER 122

QY 142 YFAICFPLRAKVVTGKRVKLVIFVIWAVAFCSAGPIFVLGVHENGTPDPTNECRPT 201
DB 123 YVACFPURAKVIITKRVKLVILWAVSFISAGPIFVLGVHENGTPDPTNECRAT 182

QY 202 EFAVRSGLLTVMWVSSIFFPVFCITVLYSLIGRKLWRRRRRGDAVVGASLRDQNHQ 261
DB 183 EYAIRSGLLTVMWISSIFFPVFCITVLYSLIGRKLWRRKKNIGSTIIRDKNNQ 242

QY 262 VKMLAVVVFAPILCWLPHFVGRYLFKSFPGSLEIAQISOYCNLVSEVLYFYLGAANP 321
DB 243 VKMLVVFVAFILCWLPHFVGRYLFKSFPAGSLEIAVISQYCNLVSEVLYFYLGAANP 302

QY 322 LYNIMSKKYRVAVFRLGFPFSPQRKSLTKDESSRAWTESSINT 366
DB 303 LYNIMSKKYRVAVACRLFGKLPKRSLSTKQDSRWVTEPTVAT 347

RESULT 8
Q6ISR8 HUMAN PRELIMINARY; PRT; 289 AA.
ID Q6ISR8_HUMAN PRELIMINARY; PRT; 289 AA.
AC Q6ISR8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Growth hormone secretagogue receptor, isoform 1b.
GN Name=GHSR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones, and Synthetic constructs;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzyski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RA Director MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [3].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Synthetic constructs;
RG NIH MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; BC069374; AAH69374.1; -; mRNA.
DR EMBL; BC069068; AAH69068.1; -; mRNA.
DR GO; 0016021; C: integral to membrane; IEA.
DR GO; 0016520; F: growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; 0004872; F: receptor activity; IEA.
DR GO; 00001584; F: growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR GO; 0007165; P: signal transduction; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 289 AA; 32153 MW; 8032FDB4C6BDD42B CRC64;

Query Match 72.9%; Score 1388; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.9e-89;
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNWNPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVAFVVGVIAG 60
DB 1 MNWNPSEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCVAFVVGVIAG 60

QY 61 NLLTMLVVSRRPRELTTNLYLSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCCKLFQ 120
DB 61 NLLTMLVVSRRPRELTTNLYLSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCCKLFQ 120

QY 121 FVSESCYATVLTITALSVERFYFAICPLRAKVVVTGRVKLVFVIWAVAFCSAGPIFV 180
DB 121 FVSESCYATVLTITALSVERFYFAICPLRAKVVVTGRVKLVFVIWAVAFCSAGPIFV 180

QY 181 LVGVEHNGTDPWDTNECRTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRLKW 240
DB 181 LVGVEHNGTDPWDTNECRTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRLKW 240

QY 241 RRRRGDAVVGASLRDQNHKQTVKML 265
DB 241 RRRRGDAVVGASLRDQNHKQTVKML 265

RESULT 9
Q7ZZJ9 CHICK
ID Q7ZZJ9 CHICK PRELIMINARY; PRT; 331 AA.
AC Q7ZZJ9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone secretagogue receptor type Ia variant.
GN Name=Ghstr1av;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=white leghorn; TISSUE=Pituitary;
RX MEDLINE=22874039; PubMed=14511992; DOI=10.1016/S0016-6480(03)00247-8;
RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Ohta Y., Tsushima N.,
RA Wakita M., Shimada K.;
RT "Molecular characterization of chicken growth hormone secretagogue
RT receptor gene";
RL Gen. Comp. Endocrinol. 134:198-202 (2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AB095996; BAC76445.1; -; mRNA.
DR EMBL; ENSG000000009187; Gallus gallus.
DR GO; 0016021; C: integral to membrane; IEA.
DR GO; 0016520; F: growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; 0004872; F: receptor activity; IEA.
DR GO; 00001584; F: rhodopsin-like receptor activity; IEA.
DR GO; 0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR GO; 0007165; P: signal transduction; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 331 AA; 37568 MW; 1BE477BF2D7A3BEB CRC64;

Query Match 68.7%; Score 1308; DB 2; Length 331;
Best Local Similarity 72.2%; Pred. No. 8.6e-84;
Matches 249; Conservative 37; Mismatches 43; Indels 16; Gaps 1;

QY 22 DASPGNDSLGDELLQLFPAPLAGVTATCVAFVVGVIAGVTATCVAFVVGVIAG 81
DB 3 EGSSENRTGGESPLRLFPAPVLTGIVACVLLFVVGVLGNLMTMLVVSFRDMRTTNFY 62

QY 82 LSSWAFSDLLIFLCMPDLVRLWQYRPNWFGDLCCKLFQFVSESCYATVLTITALSVER 141
DB 63 LSSWAFSDLLIFLCMPDLVRLWQYRPNWFGDLCCKLFQFVSESCYATVLTITALSVER 122

QY 142 YFAICPLRAKVVVTGRVKLVFVIWAVAFCSAGPIFVVGVEHNGTDPWDTNECRPT 201
DB 123 YVAICPLRAKVVITKRKVLVILWAVSFISAGPIFVVGVEHNGTDPWDTNECRAT 182

QY 202 EFVAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRLWRRRGDAVVGASLRDQNHKQT 261
DB 183 EYAIRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRLWRRKRKRGIPSTIIRDKNKQT 242

QY 262 VKMLAVVVFVAFILCWLPFHVGRVLFPSKSPFGSLLEIAIQISQYCNLVSVFLYLSAAINPI 321
DB 243 VKML-----GRYLFPSKSPFGSLLEIAIVISQYCNLVSVFLYLSAAINPI 296

QY 322 LYNNIMSKYRVAVRLLGPFPFQSRKLSLTLDKSSRAWTESSINT 366
DB 287 LYNNIMSKYRVAAACRLFGKLPKRLSKSLSSSTKQDSSRWTEPTVAT 331

RESULT 10
Q6YGZ3 ACASC
ID Q6YGZ3 ACASC PRELIMINARY; PRT; 385 AA.
AC Q6YGZ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Growth hormone secretagogue receptor 1a.
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15062547; DOI=10.1016/j.mce.2003.11.020;
RA Chan C.B., Cheng C.H.K.;
RT "Identification and functional characterization of two alternatively
spliced growth hormone secretagogue receptor transcripts from the
pituitary of black seabream *Acanthopagrus schlegelii*.";
RL Mol. Cell. Endocrinol. 214:81-95(2004).
CC -/- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -/- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC EMBL: AY151040; AN77875.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR003905; GHS1 receptor.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR01417; GHSRECEPTOR.
DR PRINTS: PR00237; GPCR RHODOPSIN.
DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 385 AA; 43697 MW; 655CBDA9702887A9 CRC64;

Query Match 58.0%; Score 1105; DB 2; Length 385;
Best Local Similarity 56.2%; Pred. No. 1.7e-69;
Matches 216; Conservative 59; Mismatches 73; Indels 36; Gaps 5;

QY 2 WNPATPEEFGFNLTADLDWDASPGNDSLGDELQLFPAPLAGVATCTVALFVVGIAGN 61
DB 17 WEETRNATKRFDLGLPLNY-----YSIPLTGITIACTLLFLVGVAGN 60
QY 62 LITMLVVSFRRLRTTNLYLSMAFSDLLIFLCPLDLVRLVQYRPNWFGDLCCKLQF 121
DB 61 VMTILVSKYRDRTTNLYLSMAVSDLLIFLCPLDLVRLVQYRPNWFGDLCCKLQF 120
QY 122 VSESCYATVLTALTSVRYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFVL 181
DB 121 VSESCYATVLTALTSVRYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFVL 180
QY 182 VGVHEH-----NGT-----DPWTNCRPTFEFAVRSGLLTVMVWVSSIFFFLPV 225
DB 181 VGVVERDSMPGNLSWYMGNGTGFPPEEGDTRECKMTHYAVESGLMGAMVWLSVFFMPV 240
QY 226 FCILTLYSLIGRLRRRRRGDAVVG-ASLRDQNHQKQTVKMLAVVVFATFLCWLPHVGRY 284
DB 241 FCILTLYSLIGRLRRRRRGDAVVG-ASLRDQNHQKQTVKMLAVVVFATFLCWLPHVGRY 300
QY 285 LFSKSPGPSLEIAQISOYCNLSVFLFYLSAANPILYNTMSKKYRVAVFRLGLGF---E 341
DB 301 LQPSRLDAPSLLSLEYCSLVSVLFLYLSAANPILYNTMSKKYRVAVFRLGLGLIDSQ 360
QY 342 PFSQRLSTLKDESSRAWTESSIN 365
DB 361 PPRGRSTASTKVGDSNGWTESTIS 384

Db 361 TVRMD---GWTESTVS 373

RESULT 12

Q4STY3 TETNG PRELIMINARY; PRT; 394 AA.

AC Q4STY3;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE Chromosome 10 SCAF14066, whole genome shotgun sequence.

DE (Fragment).

GN ORFNames=GSTENG00012720001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OX NCBI_TaxID=99883;

RN [1]

RN NUCLEOTIDE SEQUENCE.

RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

RA Aithouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,

RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,

RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

RT the early vertebrate proto-karyotype.";

RL Nature 431:946-957(2004).

RN [2]

RN NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

DR EMBL: CAEE01014066; CAP95899.1; -; Genomic_DNA.

DR InterPro: IPR003905; GHS1_receptor.

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR01417; GHSRECEPTOR.

DR PRINTS: PR00237; GPCR_RHODOPSIN.

DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.

DR PROSITE: PS02626; G-PROTEIN RECEPTOR FL 2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

FT NON TER 394

FT SEQUENCE 394 AA; 44317 MW; EBC6972602B8861D CRC64;

Query Match 56.5%; Score 1075.5; DB 2; Length 394;

Best Local Similarity 57.9%; Pred. No. 26-67;

Matches 220; Conservative 53; Mismatches 82; Indels 25; Gaps 8;

QY 4 ATPSEEPGNLTADLDW-DASPGNDSLGDE--LLQLFPAPLAGVATATCVALLFVVGAG 60

DB 21 ATCSAPVCLTAA---WRRTTPRGALSSKCHLLITQIPLLAVITACTVLTFTGVVG 77

QY 61 NLTLMLVVSFRLETTNNLYLSMAFSDLLIFLCMPDLVRLWQYRPWPNFGDLCKLFQ 120

DB 78 NVMTILVVSRYRDMRTTNNLYLSMAVSDLFIFVCMPLDLRYMRWPRMFRFGALCKLFQ 137

QY 121 FVSECTYATVLTALSVEREYAI CPELRKVVTGKRVKLVIFVWAVAFCSAGPIFV 180

DB 138 FVSECTYSTILCTALSVEREYAI CPELRKALVTKRRVRALLILLWTVSLSAGPVFV 197

QY 181 LVGVEHB-----NCTDPMDTNECRTEFAVRSGLLTVMVWVSSIFFFLPVPCLT 229

DB 198 MVGVERDSIPFTNFTSEKNGSAE-DTRECRMTQFAVESGLMEAMVWVSSVFFFPVCLT 256

QY 230 VLYSLGKRLWRRRRGDVAVG-ASLRDNHKOITVMKLVAVVFAFILLCWLPFHVCRYLPSK 288

DB 257 VLYSLIGRRLWLRRHRETSINSRVAYRDKSNROTIKMLVVVLAFLVLCWLPFHVCRYLQFR 316

QY 289 SFEPGSLIEIAISOYCNLVSVFLFYLSAANPILNYIMSKYRVAVFRLILGF---EPFSQ 345

DB 317 SLDAPSPLLSLSEYCSLVSVFLFYLSAANPILNYIMSKYRGAVARLFGVSDGHPQRG 376

QY 346 RKLSTLKDESSRAWTESSIN 365

DB 377 RTASTVKGD---GWTESTVS 393

RESULT 13

Q7ZZJ8 CHICK PRELIMINARY; PRT; 267 AA.

AC Q7ZZJ8;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Growth hormone secretagogue receptor type 1b.

GN Names=Ghsrlb;

OC Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=white leghorn; TISSUE=Pituitary;

RA Tanaka M., Miyazaki T., Yamamoto I., Nakai N., Wakita M., Shimada K.,

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC EMBL: AB095997; BC76446.1; -; mRNA.

DR Ensembl: ENSGALG0000009187; Gallus gallus.

DR GO: GO:0016021; C: integral to membrane; IEA.

DR GO: GO:0016220; F: growth hormone-releasing hormone receptor a. . . ; IEA.

DR GO: GO:0004872; F: receptor activity; IEA.

DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.

DR GO: GO:0007165; P: signal transduction; IEA.

DR InterPro: IPR003905; GHS1_receptor.

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR01417; GHSRECEPTOR.

DR PRINTS: PR00237; GPCR_RHODOPSIN.

DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.

DR PROSITE: PS02626; G-PROTEIN RECEPTOR FL 2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

FT NON TER 267

FT SEQUENCE 267 AA; 30209 MW; 00563690B35AD107 CRC64;

Query Match 53.0%; Score 1010; DB 2; Length 267;

Best Local Similarity 74.3%; Pred. No. 5.4e-63;

Matches 188; Conservative 30; Mismatches 35; Indels 0; Gaps 0;

QY 22 DASPGNDSLGDELLQLFPAPLAGVATATCVALLFVVGAGVATATVLTALSVER 81

DB 3 EGSSENRTGSGSLRFLFPAPLVLTGTVACVLLFVVGVLGMLMTMLVVSFRDMRTTNNFY 62

QY 82 LSSMAFSDLLIFLCMPDLVRLWQYRPWPNFGDLCKLFQFVSECTYATVLTALSVER 141

DB 63 LSSMAFSDLLIFLCMPDLVRLWQYRPWPNFGDLCKLFQFVSECTYSTILTALSVER 122

QY 142 YPAICPLRAKVVVTKGRVKLVIFVWAVAFCSAGPIFVWVGVHEHNGTDPWDTNECRPT 201

DB 123 YVAICPLRAKVIITRKVKLVILWVAFISAGPIFVWVGVHEHNGTNPSTNECRAT 182

QY 202 EFVRSGLLTVMVWVSSIFFFLPVPCLTLVLYSLIGRKLWRRRRGDVAVGASLRDNHKOIT 261

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Db 183 EYAIRSGLTINWVLISSIFFFLPVCLTVLSLIGRKLWRRKKNIGFSTIIRDKNNKQT 242
QY 262 VKMLAVVVFVAFIL 274
Db 243 VKMLGMAPRALCL 255

RESULT 14
Q711Q7 CHICK
ID Q711Q7 CHICK PRELIMINARY; PRT; 215 AA.
AC Q711Q7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Putative growth hormone secretagogue receptor 1a (Fragment).
GN Name=GHS1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=HYPOthalamus;
RX MEDLINE=22874034; PubMed=14511987; DOI=10.1016/S0016-6480(03)00250-8;
RA Geelissen S.M.E., Beck I.M.E., Darras V.M., Kuhn E.R.,
RA Van der Gayten S.;
RT "Distribution and regulation of chicken growth hormone secretagogue
RT receptor isoforms.";
RL Gen. Comp. Endocrinol. 134:167-174(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
EMBL; AJ309543; CAC29062.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016520; F:growth hormone-releasing hormone receptor a. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003905; GHS1_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01417; GHSRECEPTOR.
DR PRINTS; PR00237; GPCRHOODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 24487 MW; 68BCE14DFE81DEF5 CRC64;

Query Match 45.7%; Score 871; DB 2; Length 215;
Best Local Similarity 75.3%; Pred. No. 2.5e-53;
Matches 165; Conservative 19; Mismatches 19; Indels 16; Gaps 1;

QY 102 RLWQYRPNFGDLCKLQFQFSESCTYATVITITALSVERFAICFPLRAKVVTGKRVK 161
Db 1 RLWQYRPNFGDLCKLQFQFSESCTYSTILNALSVERVVAICFPLRAKVIITKRVK 60

QY 162 LVIFVIMAVAFCSAGPIFVLGVHENGTDPDWTNCEKPTSFVRSGLLTVWVWVSSIFF 221
Db 61 LVILILWAVSFISAGPIFVLGVHENGTNPLSTNECRATEFAIRSGLLTITWVWISSIFF 120

QY 222 FLPVFCLTVLSLIGRKLWRRRRGDVAVGSALRDQNHQTVKMLAVVVFVAFILCWLPFHV 281
Db 121 FLPVFCLTVLSLIGRKLWRRKKNIGSTIIRDKNNKQTKML----- 164

QY 282 GRYLFSKFEFGSLBIAIOISQYCNLVSVFLVFLSAINP 320
Db 165 GRYLFSKFEAGSLBIAIVISQYCNLVSVFLVFLSAATP 203
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RESULT 15
MTLR_HUMAN
ID AC MTLR_HUMAN STANDARD; PRT; 412 AA.
AC O43193;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Motilin receptor (G-protein coupled receptor 38).
GN Name=MLNR; Synonyms=GPR38, MTLR, MTLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM A).
RX MEDLINE=98110578; PubMed=9441746; DOI=10.1006/geno.1997.5069;
RA McKee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,
RA Hreniuk D.L., Smith R.G., Howard A.D., van der Ploeg L.H.T.;
RT "Cloning and characterization of two human G protein-coupled receptor
RT genes (GPR38 and GPR39) related to the growth hormone secretagogue and
RT neurotensin receptors.";
RL Genomics 46:426-434(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS A AND B).
RX MEDLINE=99316084; PubMed=10381885; DOI=10.1126/science.284.5423.2184;
RA Feighner S.D., Tan C.P., McKee K.K., Palyha O.C., Hreniuk D.L.,
RA Pong S.-S., Austin C.P., Figueroa D., MacNeil D., Cascieri M.A.,
RA Nargund R., Bakshi R., Abramovitz M., Stocco R., Kargman S.,
RA O'Neill G., van Der Ploeg L.H.T., Evans J., Patchett A.A., Smith R.G.,
RA Howard A.D.;
RT "Receptor for motilin identified in the human gastrointestinal
RT system.";
RL Science 284:2184-2188(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM A).
RC TISSUE=Stomach;
RA King M.W., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15057823; DOI=10.1038/nature02379;
RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,
RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,
RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,
RA Aswell R.I.S., Babbage A.K., Bagguley C.L., Bailey J., Bannerjee R.,
RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,
RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
RA Deloukas P., Dhani P., Dunham I., Dunn M., Earthworm M.E.,
RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,
RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,
RA Grafham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,
RA Hunt J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,
RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,
RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,
RA Moore M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,
RA Sehra H.K., Showkneen R., Skuce C.D., Smith M., Steward C.A.,
RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.I.;
RT "The DNA sequence and analysis of human chromosome 13.";
RL Nature 428:522-528(2004).
RN [5]
RP FUNCTION.
```

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RX MEDLINE=21219832; PubMed=11322507; DOI=10.1385/ENDO.14:1.009;
RA Smich R.G., Leonard R., Bailey A.R.T., Palyha O.C., Feighner S.D.,
RA Tan C.P., McKee K.K., Pong S.-S., Griffin P.R., Howard A.D.;
RT "Growth hormone secretagogue receptor family members and ligands.";
RL Endocrine 14:9-14(2001)
CC -!- FUNCTION: Receptor for motilin.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC Name=B;
CC IsoId=O43193-1; Sequence=Displayed;
CC IsoId=O43193-2; Sequence=VSP_001894;
CC -!- TISSUE SPECIFICITY: Expressed only in thyroid, stomach, and bone marrow.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: AF034632; AAC36081.1; -; Genomic_DNA.
CC EMBL: AY603964; AAT35806.1; -; mRNA.
CC EMBL: AL137000; CAC19107.1; -; Genomic_DNA.
CC Ensembl: ENSG00000102539; Homo sapiens.
CC HGNC: HGNC:4495; MLNR.
CC MIM: 602885; -;
CC GO: GO:0005887; C: integral to plasma membrane; TAS.
CC GO: GO:0004930; F: G-protein coupled receptor activity; TAS.
CC GO: GO:0007586; P: digestion; TAS.
CC GO: GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
CC InterPro: IPR003905; GHS1 receptor.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm1.1; 1.
CC PRINTS: PR01417; GHSRECEPTOR.
CC PRINTS: PR00237; GPCRHHODPSN.
CC PROSITE: PS00237; G-PROTEIN RECEPTOR F1_1; 1.
CC PROSITE: PS0262; G-PROTEIN RECEPTOR F1_2; 1.
CC Alternative splicing: G-protein coupled receptor; Glycoprotein;
KW Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 35 Extracellular (Potential).
FT TRANSMEM 36 56 1 (Potential).
FT TOPO_DOM 57 74 Cytoplasmic (Potential).
FT TRANSMEM 75 94 2 (Potential).
FT TOPO_DOM 95 112 Extracellular (Potential).
FT TRANSMEM 113 134 3 (Potential).
FT TOPO_DOM 135 157 Cytoplasmic (Potential).
FT TRANSMEM 158 178 4 (Potential).
FT TOPO_DOM 179 246 Extracellular (Potential).
FT TRANSMEM 247 270 5 (Potential).
FT TOPO_DOM 271 298 Cytoplasmic (Potential).
FT TRANSMEM 299 320 6 (Potential).
FT TOPO_DOM 321 334 Extracellular (Potential).
FT TRANSMEM 335 358 7 (Potential).
FT TOPO_DOM 359 412 Cytoplasmic (Potential).
FT CARBOHYD 6 6 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 192 192 N-linked (GlcNAc...) (Potential).
FT DISULFID 111 235 By similarity.
FT VARSPLIC 301 412 LVVLAFLICWLVHGVRIIYNTEDSRMMYFSQYFNVAL
FT QLFYLSINFLYNLISKYRAAFKLLARKSRPRGFHR
FT SRDTAGVAGDTGDTVGYTETSANVTMG -> RKWSRRG
FT SKDACLOSAPPTAQTGLPLAQLWAPLPAPPIPIPAS
FT TRRGSGGIYNLVALPRWQNLHKGPRFADVLLSVL
FT (in isoform B).
FT /FTId=VSP_001894.
SQ SEQUENCE 412 AA; 45344 MW; C13FF6165012DEF3 CRC64;

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Query Match 45.3%; Score 863.5; DB 1; Length 412;
 Best Local Similarity 44.7%; Pred. No. 1.5e-52;
 Matches 186; Conservative 59; Mismatches 106; Indels 65; Gaps 9;

Search completed: April 10, 2006, 17:33:35
 Job time : 222.509 secs

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QY 2 WNATPSEEPGNLTADLDWDASPGNDSLGDELLQLFPAPLAGVATATCVAFVVGVIAGN 61
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
5 WNGSDGPEGA-----REPPWALPPCD---ERRCSPFPLGALVPVTAVCLCLFVVGVS 56
QY 62 LLTMLVSRFRRLRTTNLYLSSMAFSDLLIFLCWPLDLVRLMQVRPNWFGDLLCKLP 121
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
57 VVTVMILIGRYDRMETTNLYLGSMAVSDLLILGLPFDLYRLWRSRPVWFGPLLCRLSL 116
QY 122 VSECTVATVITATLSVERYPALCFPLRAKVVTKGRVKLVIFVIMAVAFCSAGPIF 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
117 VEGCTVATLHMTALSVRYLAICRPLRAVLTTRRRVRLIAVLWALLSAGPFLFL 176
QY 182 VGVHE-----NGT-----DP--W-----DTNECR 199
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
177 VGVQDPGISVVPGLNGTARIASSPLASSPPLLSRAPPPSPSPGPTAAEAALFSR 236
QY 200 PTEFAVRSGLLTVMVWVSSIFPFLPVCLTVLYSLIGKLRWRRGDAVGCASLRDQ 259
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
237 PS--PAQLGALRVMLWVTAYFFFLCLSLYGLIGRELWSSRRPLRGPAASGRGR 294
QY 260 QTVKMLAVVPAFILCWLPHVGRYLFSSKSPSGSLEIAQISQYCNLVSVFLYLSA 319
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
295 QTVRVLLVVLAFIICWLPFHVGRIIYNTEDS---RMVFSQYFNIVLQLFYLSA 351
QY 320 PILYNIMSKYRVAVFRLLGPEPFSQRKLSLTKDESSR-----AMTESSIN 365
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
352 PILYNLISKYRAAAAFKLLARKSRPRGFHRSRDTAGEVAGDTGDTVGYTETSAN 407

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 10, 2006, 17:23:48 ; Search time 205.354 Seconds
(without alignments)
783.099 Million cell updates/sec

Title: US-09-718-803A-5
Perfect score: 1905
Sequence: 1 MWNA TPSEPGFNLTLADLD.....KSLTKDESGRAWTESSINT 366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1905	100.0	366	3 AAY70345	Aay70345 Human G p
2	1905	100.0	366	3 AAY90632	Aay90632 Human G p
3	1905	100.0	366	4 AAB97376	Aab97376 Rat growt
4	1905	100.0	366	4 AAB62650	Aab62650 Human G-p
5	1905	100.0	366	5 ABB09534	Abb09534 Human ghr
6	1905	100.0	366	7 ADC22607	Adc22607 Human G p
7	1905	100.0	366	7 ADH14080	Adh14080 Human GHS
8	1905	100.0	366	8 ADD35398	Add35398 Human gro
9	1905	100.0	366	8 ADN12078	Adn12078 Protein #
10	1905	100.0	366	8 ADN11756	Adn11756 Human gro
11	1905	100.0	366	8 ADO29025	Ado29025 Human nov
12	1905	100.0	366	8 ADQ28857	Adq28857 Human ghr
13	1899	99.7	366	3 AAY90666	Aay90666 Human mut
14	1899	99.7	366	7 ADC22729	Adc22729 Human G p
15	1899	99.7	366	7 ADH14202	Adh14202 Murated h
16	1874	98.4	361	2 AAW19217	Aaw19217 Human gro
17	1874	98.4	362	2 AAW19610	Aaw19610 Human gro
18	1789	93.9	364	4 AAB97377	Aab97377 Rat growt
19	1788	93.9	364	3 AAY54565	Aay54565 A mouse g
20	1788	93.9	364	8 ADO29026	Ado29026 Mouse nov
21	1782	93.5	364	2 AAW19613	Aaw19613 Rat growt
22	1770	92.9	364	2 AAW19220	Aaw19220 Rat growt
23	1713.5	89.9	705	8 ADU82862	Adu82862 Ligand up
24	1704	89.4	353	2 AAW19215	Aaw19215 Swine gro

ALIGNMENTS

RESULT 1
AAY70345
ID AAY70345 standard; protein; 366 AA.
XX AC AAY70345;
XX 20-JUN-2000 (first entry)
XX Human G protein-coupled orphan receptor, GHSR.
DE Human G protein-coupled orphan receptor; GPCR; agonist; G protein; treatment;
KW GPCR fusion protein; inverse agonist; drug; GHSR; human.
XX Homo sapiens.
XX WO200006597-A2.
XX 10-FEB-2000.
XX 30-JUL-1999; 99WO-US017425.
XX 31-JUL-1998; 98US-0094879P.
PR 30-OCT-1998; 98US-0106300P.
PR 04-DEC-1998; 98US-0110906P.
PR 26-FEB-1999; 99US-0121851P.
PA (AREN-) ARENA PHARM INC.
XX Behan DP, Chalmers DT, Liaw C, Lin I, Lowitz K, Chen R;
WPI; 2000-195260/17.
N-PSDB; AAZ51463.
XX Identification of a compound useful as a therapeutic agent, comprises
identifying a compound against constitutively activated G protein-coupled
orphan receptors.
XX Example 2; Page 123; 123pp; English.
CC The patent discloses a method of identifying agonists and inverse or
partial agonists to the endogenous, constitutively activated G protein-
coupled orphan receptors (GPCRs), by contacting them with a GPCR fusion
protein comprising a GPCR and a G protein. Determining expression of
GPCRs in tissue samples can be used to identify related diseases. Inverse
agonists to these receptors can be used as drugs for treating GPCR-
related diseases. The present protein sequence is that of human G protein
-coupled orphan receptor, GHSR

```

XX SQ Sequence 366 AA;
Query Match 100.0%; Score 1905; DB 3; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNATPSEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFVVGAG 60
DB 1 MNATPSEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFVVGAG 60
QY 61 NLLTMLVVSRRFRLTTNLYLSSMAFSDLLIFLCMPDLDLVRLMQRPNWFGDILLCKLFQ 120
DB 61 NLLTMLVVSRRFRLTTNLYLSSMAFSDLLIFLCMPDLDLVRLMQRPNWFGDILLCKLFQ 120
QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
QY 181 LVGVEHNGTDPWDTNECRPTFEFVRSGLLTVWVWSSIFFPLPVFCLTVLYSLGRKLM 240
DB 181 LVGVEHNGTDPWDTNECRPTFEFVRSGLLTVWVWSSIFFPLPVFCLTVLYSLGRKLM 240
QY 241 RRRRGDAVVGASLRDQNHQKQTVKMLAVVVFAPILCWLPHVGRYLFKSFPGSLEIAQI 300
DB 241 RRRRGDAVVGASLRDQNHQKQTVKMLAVVVFAPILCWLPHVGRYLFKSFPGSLEIAQI 300
QY 301 SQYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLGFPFSGQRKSLTLKDESSRAWT 360
DB 301 SQYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLGFPFSGQRKSLTLKDESSRAWT 360
QY 361 ESSINT 366
DB 361 ESSINT 366

RESULT 2
AA90632
ID AA90632 standard; protein; 366 AA.
AC AA90632;
XX 21-AUG-2000 (first entry)
DE Human G protein-coupled receptor GHSR.
KW G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;
KW antagonist.
XX Homo sapiens.
XX WO200022129-A1.
XX 20-APR-2000.
PF 12-OCT-1999; 99WO-US023938.
XX 13-OCT-1998; 98US-00170496.
XX (AREN-) ARENA PHARM INC.
XX Behan DP, Chalmers DT, Liaw CW;
XX WPI; 2000-329165/28.
DR N-PSDB; AAA30643.
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents.
XX Example 1; Page 167-169; 341pp; English.
XX

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CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AA90643-
CC AA90677 and AA90683-190687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence X-
CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
CC Ala, and is preferably Lys. When the endogenous residue at this position
CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
CC amino acid stretch between the substituted amino acid and the pro may be
CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC residues. The constitutively active GPCRs are useful for identifying
CC antagonists, agonists and partial agonists for use as pharmaceutical
CC agents. The mutant proteins are also useful in research settings for
CC elucidating the roles of the receptors in normal and diseased conditions.
CC Antagonists for a particular GPCR are useful for treating diseases and
CC disorders associated with that receptor. Because the novel mutant GPCRs
CC are constitutively active, they can be used directly for screening of
CC compounds without the need for endogenous ligands. The present sequence
CC represents a human wild-type GPCR referred to in an exemplification of
CC the invention
XX SQ Sequence 366 AA;
Query Match 100.0%; Score 1905; DB 3; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNATPSEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFVVGAG 60
DB 1 MNATPSEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFVVGAG 60
QY 61 NLLTMLVVSRRFRLTTNLYLSSMAFSDLLIFLCMPDLDLVRLMQRPNWFGDILLCKLFQ 120
DB 61 NLLTMLVVSRRFRLTTNLYLSSMAFSDLLIFLCMPDLDLVRLMQRPNWFGDILLCKLFQ 120
QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
QY 181 LVGVEHNGTDPWDTNECRPTFEFVRSGLLTVWVWSSIFFPLPVFCLTVLYSLGRKLM 240
DB 181 LVGVEHNGTDPWDTNECRPTFEFVRSGLLTVWVWSSIFFPLPVFCLTVLYSLGRKLM 240
QY 241 RRRRGDAVVGASLRDQNHQKQTVKMLAVVVFAPILCWLPHVGRYLFKSFPGSLEIAQI 300
DB 241 RRRRGDAVVGASLRDQNHQKQTVKMLAVVVFAPILCWLPHVGRYLFKSFPGSLEIAQI 300
QY 301 SQYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLGFPFSGQRKSLTLKDESSRAWT 360
DB 301 SQYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLGFPFSGQRKSLTLKDESSRAWT 360
QY 361 ESSINT 366
DB 361 ESSINT 366

RESULT 3
AA907376
ID AA907376 standard; protein; 366 AA.
XX AA907376;
XX 16-AUG-2001 (first entry)
DE Rat growth hormone secretagogue receptor (GHSR) related protein.
XX Growth hormone secretagogue receptor; GHSR; GHSR ligand; nootropic;
KW antiarthritic; cytostatic; antidiabetic; pituitary dwarfism;
KW Turner's syndrome; chronic nephritis; chondrodystrophy; Down's syndrome;
KW Silver syndrome; bone formation disorder; juvenile chronic arthritis;
XX

```

KW megacephalia; tumour; insulinoma; calcinoid; diabetes; rat.

OS Rattus sp.

PN WO200132705-A1.

XX PD 10-MAY-2001.

XX PF 31-OCT-2000; 2000WO-JP007635.

XX PR 01-NOV-1999; 99JP-00311632.

XX PR 17-DEC-1999; 99JP-00358723.

XX XX (TAKE) TAKEDA CHEM IND LTD.

XX PI Hinuma S, Kawamata Y, Fukusumi S, Fujii R;

XX XX WPI; 2001-308741/32.

XX DR Growth-hormone secretagogue receptor ligand polypeptides and encoded DNAs, useful in diagnosis and screening drug candidates for treating e.g. pituitary dwarfism, Turner syndrome, chronic nephritis.

XX PS Claim 14; Page 90-92; 106pp; Japanese.

XX CC This invention relates to a growth hormone secretagogue receptor (GHSR) ligand peptide. The invention contains bovine, human, rat and porcine GHSR gene and protein sequences, and also GHSR ligand sequences. The use of an antibody directed against GHSR ligand, GHSR promoters and inhibitors may lead to nootropic, antiarthritic, cytostatic, and antidiabetic activity. GHSR DNA, protein, promoters and inhibitors are useful for preventing or treating diseases caused by insufficient growth hormone, e.g. pituitary dwarfism, Turner syndrome, chronic nephritis, chondrodysplasia, adult pituitary failure, Down's syndrome, Silver syndrome, bone formation disorder, juvenile chronic arthritis syndrome or for diseases of megacephalia, thyroid stimulating hormone (TSH)-promoting tumours, non-secretory (non-functional) pituitary tumours, ectopic adrenocorticotrophic hormone (ACTH)-producing tumours, myeloid thryoma, vasotrophic inhibitory peptide (VIP)-producing tumours, glucagon-producing tumour, gastrin-producing tumour, insulinoma, calcinoid, insulin-dependent or non-dependent diabetes. The present sequence represents rat GHSR-related protein

XX SQ Sequence 366 AA;

Query Match 100.0%; Score 1905; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200; Mismatches 0; Indels 0; Gaps 0;
Matches 366; Conservative 0;

Qy 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGAG 60

Db 1 MNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGAG 60

Qy 61 NLLTMLVVSRRPRELRTTNLYLSSNAFSDLLIFLCMPDLVRLNQYRPNFPGDILCKLFQ 120

Db 61 NLLTMLVVSRRPRELRTTNLYLSSNAFSDLLIFLCMPDLVRLNQYRPNFPGDILCKLFQ 120

Qy 121 FVSESCYATVLTITALSVERFYFAICPLRAKVVTVGRVKLVFIWVAVAFCSAGPIFV 180

Db 121 FVSESCYATVLTITALSVERFYFAICPLRAKVVTVGRVKLVFIWVAVAFCSAGPIFV 180

Qy 181 LVGVEHENGTDPMWTECRPEFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 240

Db 181 LVGVEHENGTDPMWTECRPEFAVRSGLLTVMVWSSIFPFLPVFCLTVLYSLIGRKLW 240

Qy 241 RRRRGDAVVGASLRDQNHQKQVTKMLAVVVFALICWLPFHVGRYLFKSPFGSLTAQI 300

Db 241 RRRRGDAVVGASLRDQNHQKQVTKMLAVVVFALICWLPFHVGRYLFKSPFGSLTAQI 300

Qy 301 SOYCNLVSVFLFYLSAANPILYNIMSKYKRVAVFRLIGPEPFSQKSLTKDESSRAWT 360

Db 301 SOYCNLVSVFLFYLSAANPILYNIMSKYKRVAVFRLIGPEPFSQKSLTKDESSRAWT 360

Qy 361 ESSINT 366
Db 361 ESSINT 366
RESULT 4
AAB62650
ID AAB62650 standard; protein; 366 AA.
XX AC AAB62650;
XX XX 23-JUL-2001 (first entry)
XX DE Human G-protein coupled receptor, GHS-R.
XX KW zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
KW G-protein coupled receptor.
XX OS Homo sapiens.

Key	Location/Qualifiers
FT Domain	1..40
FT Domain	/note= "extracellular domain"
FT Domain	41..66
FT Domain	/note= "transmembrane alpha-helix 1"
FT Domain	67..72
FT Domain	/note= "cytoplasmic fragment"
FT Domain	73..96
FT Domain	/note= "transmembrane alpha-helix 2"
FT Domain	97..117
FT Domain	/note= "extracellular domain"
FT Domain	118..139
FT Domain	/note= "transmembrane alpha-helix 3"
FT Domain	140..162
FT Domain	/note= "cytoplasmic fragment"
FT Domain	163..183
FT Domain	/note= "transmembrane alpha-helix 4"
FT Domain	184..211
FT Domain	/note= "extracellular domain"
FT Domain	212..235
FT Domain	/note= "transmembrane alpha-helix 5"
FT Domain	236..263
FT Domain	/note= "cytoplasmic fragment"
FT Domain	264..285
FT Domain	/note= "transmembrane alpha-helix 6"
FT Domain	286..302
FT Domain	/note= "extracellular domain"
FT Domain	303..326
FT Domain	/note= "transmembrane alpha-helix 7"
FT Domain	327..326
FT Domain	/note= "cytoplasmic fragment"

WO200138355-A2.

31-MAY-2001.

22-NOV-2000; 2000WO-US032074.

22-NOV-1999; 99US-0166765P.

(ZYMO) ZYMOGENETICS INC.

Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

WPI; 2001-355879/37.

N-PSDB; AAF83680.

Forming reversible peptide receptor complex for purifying cell and peptides, stimulating signal transduction and modulating hormone secretion, involves contacting a receptor with zsig33 polypeptide.

XX Claim 2; Page 95-98; 11pp; English.

PS The invention relates to a method of forming a reversible peptide-

XX receptor complex that involves providing an immobilized receptor, and

CC contacting the receptor with a zsig33 peptide (comprising residues 24-37

CC of AAB62649), where the receptor binds to the zsig33 peptide. The method

CC is useful for purifying cells, purifying a peptide, stimulating signal

CC transduction in a cell expressing a receptor. It is also useful for

CC modulating secretion of hormones, neural development and/or utilization,

CC gastric contractility, nutrient uptake, secretion of digestive and

CC pancreatic enzymes and hormones, secretion of insulin-like growth factor

CC -1, secretion of non-zsig33 proteins. It is useful for modulating growth

CC hormone secretion in a mammal having a disease associated with abnormal

CC levels of growth hormone, such as osteoporosis, bone repair, bone

CC remodeling, low osteoblast levels, cartilage repair and remodeling,

CC skeletal dysplasia, immune suppression, obesity, growth retardation,

CC protein catabolic responses after surgery, cachexia, protein loss,

CC dwarfism, wound healing and ovulation induction, treating a mammal having

CC a metabolic disorder requiring neurological feedback, such as satiety

CC regulation, glucose absorption and metabolism and neuropathy-associated

CC gastrointestinal disorders, and stimulating glucose-induced insulin

CC release in a mammal. The present sequence represents the human G-protein

CC coupled receptor, GHS-R, to which the zsig33 peptide binds to

XX

SQ Sequence 366 AA;

Query Match 100.0%; Score 1905; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNATPSEPGNLTADLDWDASPGNDSLGDELLQLPAPLLAGVTATCVAFVVGAG 60
|||||
DB 1 MNNATPSEPGNLTADLDWDASPGNDSLGDELLQLPAPLLAGVTATCVAFVVGAG 60
|||||

QY 61 NLLTMLVWSRPRELRTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLFPQ 120
|||||
DB 61 NLLTMLVWSRPRELRTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLFPQ 120
|||||

QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRKLVIFVIWAVAFCSAGPIFV 180
|||||
DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRKLVIFVIWAVAFCSAGPIFV 180
|||||

QY 181 LVGVEHNGTDPWDNECRPTFEAVRSGLLTVMWVSSIFFFLPVFCULTVLYSLGRKLW 240
|||||
DB 181 LVGVEHNGTDPWDNECRPTFEAVRSGLLTVMWVSSIFFFLPVFCULTVLYSLGRKLW 240
|||||

QY 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIEIAQI 300
|||||
DB 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIEIAQI 300
|||||

QY 301 SOYCNLVSVFLPYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360
|||||
DB 301 SOYCNLVSVFLPYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360
|||||

QY 361 ESSINT 366
|||||
DB 361 ESSINT 366
|||||

RESULT 5
ABB09534
ID ABB09534 standard; protein; 366 AA.
XX
XX ABB09534;
AC
XX
DT 22-OCT-2002 (first entry)
XX Human ghrelin receptor (GHSR, growth hormone secretagogue receptor).
DE Human; ghrelin receptor; appetite; food intake; agonist; analogue;
KW undernutrition; anorexia; cachexia; malignant disease; infection;
KW inflammatory disease; weight loss; antagonist; obesity; anorectic;
KW

KW anabolic; GHSR; growth hormone receptor; GHSR; receptor.

XX Homo sapiens.

OS WO200260472-A1.

XX 08-AUG-2002.

PD 31-JAN-2002; 2002WO-JP000765.

PF 31-JAN-2001; 2001JP-00024423.

PR (CHUS) CHUGAI SEIYAKU KK.

XX Inui A, Asakawa A, Kaga T;
WIPI; 2002-619206/66.

XX Remedies for diseases with hypo-nutrition status e.g. inappetence and
cachexia, containing ghrelin or its analogs including agonists and
antagonists.

PT Disclosure; Fig 1B; 50pp; Japanese.

XX The invention relates to the use of ghrelin or its analogues for the
treatment of diseases associated with undernutrition such as anorexia,
and also relates to the use of ghrelin antagonists for the prevention or
treatment of obesity. The invention additionally discloses a method for
screening ghrelin agonists or antagonists by measuring the amount of food
intake, neuropeptide Y (NPY) expression, binding of NPY to NPY receptor
Y1, oxygen consumption, gastric emptying, or activity of the vagus nerve.
Intracerebroventricular (ICV) administration of ghrelin in animals was
found to increase food intake over a period of 24 hours. Ghrelin and its
analogues may therefore be used to treat conditions such as loss of
appetite, anorexia, cachexia, malignant diseases, and weight loss
associated with infection or inflammatory diseases. Conversely, ghrelin
antagonists may be used in the treatment of obesity. The present sequence
represents the human ghrelin receptor (also known as growth hormone
secretagogue receptor, or GHSR) which is referred to in the disclosure of
the invention

XX

SQ Sequence 366 AA;

Query Match 100.0%; Score 1905; DB 5; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNATPSEPGNLTADLDWDASPGNDSLGDELLQLPAPLLAGVTATCVAFVVGAG 60
|||||
DB 1 MNNATPSEPGNLTADLDWDASPGNDSLGDELLQLPAPLLAGVTATCVAFVVGAG 60
|||||

QY 61 NLLTMLVWSRPRELRTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLFPQ 120
|||||
DB 61 NLLTMLVWSRPRELRTTNLYLSSMAFSDLLIFLCMPLDLVRLWQYRPNWFGDLCKLFPQ 120
|||||

QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRKLVIFVIWAVAFCSAGPIFV 180
|||||
DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRKLVIFVIWAVAFCSAGPIFV 180
|||||

QY 181 LVGVEHNGTDPWDNECRPTFEAVRSGLLTVMWVSSIFFFLPVFCULTVLYSLGRKLW 240
|||||
DB 181 LVGVEHNGTDPWDNECRPTFEAVRSGLLTVMWVSSIFFFLPVFCULTVLYSLGRKLW 240
|||||

QY 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIEIAQI 300
|||||
DB 241 RRRRGDAVVGASLRDNKHQTVKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIEIAQI 300
|||||

QY 301 SOYCNLVSVFLPYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360
|||||
DB 301 SOYCNLVSVFLPYLSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKSLTLKDESSRAWT 360
|||||

QY 361 ESSINT 366
|||||

Db 361 ESSINT 366

RESULT 6

ADC22607

ID ADC22607 standard; protein; 366 AA.

AC ADC22607;

XX 18-DEC-2003 (first entry)

DT Human G protein-coupled receptor (GPCR) polypeptide #24.

DE Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;

XX intracellular-3 region; IC3; receptor.

KW Homo sapiens.

XX US6553339-B1.

PN 29-APR-2003.

PD 13-OCT-1998; 98US-00170496.

PF 14-APR-1997; 97US-00839449.

PR 14-APR-1998; 98US-00060188.

PR 26-JUN-1998; 98US-0090783P.

PR 07-AUG-1998; 98US-0095677P.

XX (AREN-) ARENA PHARM INC.

PA Liaw CW, Behan DP, Chalmers DT;

XX WPI; 2003-742861/70.

PI N-PSDB; ADC22606.

DR Creating a constitutively active version of an endogenous human G protein

PT coupled receptor (GPCR) comprises substituting a specific amino acid in

PT the transmembrane-6 region with a different amino acid, and testing for

PT constitutive activity.

XX Example 1; SEQ ID NO 88; 221pp; English.

PS The invention relates to a method for treating a non-endogenous,

CC constitutively active version of an endogenous human G protein-coupled

CC receptor (GPCR) that has a transmembrane-6 (TM6) region and an

CC intracellular-3 (IC3) region, by substituting a specific amino acid in

CC the TM6 region with a different amino acid, and testing for constitutive

CC activity. The method is useful for creating a constitutively active

CC version of an endogenous human GPCR that comprises a transmembrane 6

CC region and an intracellular loop 3 region. The altered human GPCR

CC polypeptides are useful for screening test compounds for identification

CC of inverse agonists or partial agonists of GPCR polypeptides, which may

CC have therapeutic uses. The altered GPCRs may also be used in vivo or in

CC vitro in biological research. A nucleic acid encoding the altered GPCR

CC may be used to create a transgenic animal expressing the altered GPCR.

CC The method allows screening for compounds that modulate the activity of a

CC human G protein-coupled receptor without the need for provision of a

CC ligand for the receptor. This is particularly useful in allowing

CC screening of compounds against orphan receptors for which no ligand is

CC currently known. This sequence represents a human GPCR polypeptide of the

CC invention.

XX Sequence 366 AA;

SQ

Query Match 100.0%; Score 1905; DB 7; Length 366;

Best Local Similarity 100.0%; Pred. No. 1.3e-200;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNWATPSEEGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCTVALFVVGAG 60

DB 1 MNWATPSEEGFNLTADLDWDASPGNDSLGDELLQLFPAPLAGVTATCTVALFVVGAG 60

61 NLLTMLVVSFRPRELRTTTNLYLSSMAFSDLLIFLCMPDLDLVRLWQYRPMWFGDLLCKLFQ 120

61 NLLTMLVVSFRPRELRTTTNLYLSSMAFSDLLIFLCMPDLDLVRLWQYRPMWFGDLLCKLFQ 120

121 FVSESCYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIVAWAFCSAGPIFV 180

121 FVSESCYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIVAWAFCSAGPIFV 180

181 LVGVEHENGTDPDWTECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLVLSLIGRKLW 240

181 LVGVEHENGTDPDWTECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLVLSLIGRKLW 240

241 RRRRGDAVVGASLRDQNHKQTVKMLAVVFAFILCWLPHFVGRYLFKSPFSGSLEIAQI 300

241 RRRRGDAVVGASLRDQNHKQTVKMLAVVFAFILCWLPHFVGRYLFKSPFSGSLEIAQI 300

301 SOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLLGPEFPFSQRLSTLKDESSRAWT 360

301 SOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLLGPEFPFSQRLSTLKDESSRAWT 360

361 ESSINT 366

361 ESSINT 366

RESULT 7

ADH14080

ID ADH14080 standard; protein; 366 AA.

XX AC ADH14080;

XX 11-MAR-2004 (first entry)

DT Human GHSR.

DE human; non-endogenous; G protein-coupled receptor; GPCR; receptor.

XX Homo sapiens.

XX US2003105292-A1.

PN 05-JUN-2003.

PD 20-SEP-2002; 2002US-00251385.

PF 26-JUN-1998; 98US-0090783P.

PR 07-AUG-1998; 98US-0095677P.

PR 13-OCT-1998; 98US-00170496.

XX (LIAW/) LIAW C W.

PA (BEHA/) BEHAN D P.

PA (CHAL/) CHALMERS D T.

XX Liaw CW, Behan DP, Chalmers DT;

PI WPI; 2003-801247/75.

DR N-PSDB; ADH14079.

XX New constitutively active, non-endogenous version of an endogenous human

PT G protein-coupled receptor for the identification of therapeutic

PT compounds, such as agonists.

XX Example 1; SEQ ID NO 88; 227pp; English.

PS The invention relates to a constitutively active, non-endogenous version

CC of an endogenous human G protein-coupled receptor (GPCR). The GPCR is

CC used for screening therapeutic compounds as inverse agonists, agonists or

CC partial agonists. The GPCR can be also be used to elucidate and

CC understand the roles of GPCRs in normal and diseased humans. The GPCR

CC need not be purified and isolated to be used to screen for therapeutic

CC compounds. The utility of the GPCR as a research tool is enhanced because

CC the role of a particular receptor can be understood before the endogenous

CC ligand is identified. The present sequence is used in the exemplification

CC	of the present invention.	PS	Disclosure; SEQ ID NO 2; 115pp; English.
XX		XX	
SQ	Sequence 366 AA;	CC	The invention relates to a novel method for screening for therapeutic agents useful in treating a disease consisting of cancer, respiratory diseases, genito-urinary diseases, haematological diseases, cardiovascular diseases or CNS diseases in a mammal. The method comprises contacting a test compound with a growth hormone secretagogue receptor (GHS) polypeptide, and detecting binding of the test compound to the GHS polypeptide. The method of the invention has cytostatic, cardiatic, neuroprotective, respiratory, and gynaecological activity. The method is useful for screening for therapeutic agents for treating a disease consisting of cancer, respiratory diseases, genito-urinary diseases, haematological diseases, cardiovascular diseases or CNS diseases in a mammal. The present sequence represents the human GHS receptor of the invention.
QY	1 MNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60	SQ	Sequence 366 AA;
Db	1 MNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60	Query Match	100.0%; Score 1905; DB 8; Length 366;
QY	61 NLLTMLVSVRFRELTNTNLYSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQ 120	Best Local Similarity	100.0%; Pred. No. 1.3e-200;
Db	61 NLLTMLVSVRFRELTNTNLYSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQ 120	Matches 366; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	121 FVSECTYATVLTITALSVERYFAICFPPLRAKVVTGKRVKLVIVIVAWAFCSAGPIFV 180	QY	1 MNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
Db	121 FVSECTYATVLTITALSVERYFAICFPPLRAKVVTGKRVKLVIVIVAWAFCSAGPIFV 180	Db	1 MNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
QY	181 LVGVHEHGTDPWDNECRPTFEAVRSGLLTMVWVSSIFFPFLPVFCLTVLSLIGRKLW 240	QY	61 NLLTMLVSVRFRELTNTNLYSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQ 120
Db	181 LVGVHEHGTDPWDNECRPTFEAVRSGLLTMVWVSSIFFPFLPVFCLTVLSLIGRKLW 240	Db	61 NLLTMLVSVRFRELTNTNLYSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQ 120
QY	301 SOYCNLVSVFLPYLSAANPILYNIMSKYRVAVFRLGFEFPSQKSLTLKDESSRAWT 360	QY	121 FVSECTYATVLTITALSVERYFAICFPPLRAKVVTGKRVKLVIVIVAWAFCSAGPIFV 180
Db	301 SOYCNLVSVFLPYLSAANPILYNIMSKYRVAVFRLGFEFPSQKSLTLKDESSRAWT 360	Db	121 FVSECTYATVLTITALSVERYFAICFPPLRAKVVTGKRVKLVIVIVAWAFCSAGPIFV 180
QY	361 ESSINT 366	QY	181 LVGVHEHGTDPWDNECRPTFEAVRSGLLTMVWVSSIFFPFLPVFCLTVLSLIGRKLW 240
Db	361 ESSINT 366	Db	181 LVGVHEHGTDPWDNECRPTFEAVRSGLLTMVWVSSIFFPFLPVFCLTVLSLIGRKLW 240
RESULT 8		QY	241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFSKSFEPGSLERIAQI 300
ADD35398		Db	241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFSKSFEPGSLERIAQI 300
ID	ADD35398 standard; protein; 366 AA.	QY	301 SOYCNLVSVFLPYLSAANPILYNIMSKYRVAVFRLGFEFPSQKSLTLKDESSRAWT 360
AC	ADD35398;	Db	301 SOYCNLVSVFLPYLSAANPILYNIMSKYRVAVFRLGFEFPSQKSLTLKDESSRAWT 360
XX		QY	361 ESSINT 366
DT	15-JAN-2004 (first entry)	Db	361 ESSINT 366
DE	Human growth hormone secretagogue receptor SEQ ID NO:2.	RESULT 9	
KW	human; growth hormone secretagogue receptor; GHS; cancer; respiratory; genito-urinary; haematological; cardiovascular; CNS; cytostatic; cardiatic; neuroprotective; respiratory; gynaecological.	ADN12078	
XX		ID	ADN12078 standard; protein; 366 AA.
OS	Homo sapiens.	XX	
XX		XX	
PN	WO2003081258-A2.	AC	ADN12078;
XX		XX	
PD	02-OCT-2003.	DT	17-JUN-2004 (first entry)
PF	14-MAR-2003; 2003WO-BF002688.	XX	
XX		DE	Protein #3 associated with growth hormone secretagogue receptor.
PR	26-MAR-2002; 2002EP-00006653.	XX	
XX		KW	diabetes; growth hormone secretagogue receptor; GHS-R; Antidiabetic;
PA	(FARB) BAYER AG.	KW	Anorectic; obesity; blood sugar level; appetite.
PI	Golz S, Brueggemeier U, Geerts A;	XX	
XX		OS	Homo sapiens.
XX		XX	
DR	WPI: 2004-011536/01.	XX	
DR	N-PSDB; ADD35397.	PN	WO2004004772-A1.
XX		XX	
PT	Screening for therapeutic agents for treating e.g., cancer in a mammal by contacting a test compound with a growth hormone secretagogue receptor (GHS) polypeptide and detecting binding of the test compound to the GHS polypeptide.	PD	15-JAN-2004.
PT		XX	
PT		PF	03-JUL-2003; 2003WO-JP008482.
XX		XX	
XX		PR	05-JUL-2002; 2002JP-00197582.

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XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Inui A, Asakawa A;
XX DR WPI; 2004-099347/10.
XX PT Growth hormone secretagogue receptor antagonist for treatment of
XX PT diabetes, obesity and appetite control.
XX PS Disclosure; SEQ ID NO 3; 44pp; Japanese.
XX CC The present invention relates to a treatment and preventative agent for
XX CC diabetes comprises growth hormone secretagogue receptor (GHS-R)
XX CC antagonist. For treatment and prevention of diabetes, obesity, for
XX CC lowering blood sugar levels and for use in controlling appetite. The
XX CC present sequence represents a protein associated with growth hormone
XX CC secretagogue receptor.
XX SQ Sequence 366 AA;
Query Match 100.0%; Score 1905; DB 8; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MWNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
Db 1 MWNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
Qy 61 NLLTMLVVSRRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Db 61 NLLTMLVVSRRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Qy 121 FVSESCYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVFVIVWAVAFCSAGPIFV 180
Db 121 FVSESCYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVFVIVWAVAFCSAGPIFV 180
Qy 181 LVGVEHENGTDPMWDTNECRPTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLW 240
Db 181 LVGVEHENGTDPMWDTNECRPTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLW 240
Qy 241 RRRRGDAVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPFPGSLEIAQI 300
Db 241 RRRRGDAVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPFPGSLEIAQI 300
Qy 301 SQYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPEPFSQKSLTKDESSRAWT 360
Db 301 SQYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPEPFSQKSLTKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366
RESULT 10
ADN11756
ID ADN11756 standard; protein; 366 AA.
XX AC ADN11756;
XX DT 15-JUL-2004 (first entry)
XX DE Human growth hormone secretagogue GHS-R.
XX KW human; zsig33; body weight; body mass; antibody; antagonist;
XX KW gastrointestinal; antiinflammatory; antidiabetic; antitumor;
XX KW growth hormone secretagogue; GHS-R; peptide-antibody complex.
XX OS Homo sapiens.
XX PN WO2004033645-A2.
XX PD 22-APR-2004.
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XX PF 06-OCT-2003; 2003WO-US031804.
XX PR 07-OCT-2002; 2002US-0416918P.
XX PA (Zymo ) ZYMOGENETICS INC.
XX PI Jaepers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
XX DR WPI; 2004-340913/31.
XX DR N-PSDB; ADN11755.
XX PT Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
XX PT inhibiting signal transduction in a cell expressing a growth hormone
XX PT secretagogue receptor, or treating a metabolic disorder.
XX PS Disclosure; Page 91-92; 100pp; English.
XX CC The present invention relates to the use of a zsig33 peptide for forming
XX CC a peptide-antibody complex, purifying a peptide, inhibiting signal
XX CC transduction in a cell expressing a growth hormone secretagogue receptor
XX CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
XX CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a
XX CC mammal, or treating a metabolic disorder. The peptide is useful for
XX CC forming a peptide-antibody complex, purifying a peptide, inhibiting
XX CC signal transduction in a cell expressing a GHS-R, decreasing fat
XX CC growth hormone secretion in pituitary cells of a mammal, or treating a
XX CC metabolic disorder. The zsig33 polypeptides can be used to study
XX CC proliferation or differentiation in stomach, lung, pituitary,
XX CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,
XX CC skeletal muscle or pancreas. They are also useful in delivering
XX CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists are
XX CC also useful for promoting wound healing. The polypeptides, nucleic acids
XX CC and antibodies are useful for diagnosing, treating or preventing
XX CC disorders associated with gastric reflux, gastroparesis, modulation of
XX CC secretion of pituitary hormones, including growth hormone, Cohn's
XX CC disease, metabolic wasting, gastric ulcers, weight management, or
XX CC degenerative disease. The present sequence is the human GHS-R protein
XX CC sequence.
XX SQ Sequence 366 AA;
Query Match 100.0%; Score 1905; DB 8; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MWNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
Db 1 MWNATPSEEPGFNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVALFVVGIAQ 60
Qy 61 NLLTMLVVSRRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Db 61 NLLTMLVVSRRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
Qy 121 FVSESCYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVFVIVWAVAFCSAGPIFV 180
Db 121 FVSESCYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVFVIVWAVAFCSAGPIFV 180
Qy 181 LVGVEHENGTDPMWDTNECRPTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLW 240
Db 181 LVGVEHENGTDPMWDTNECRPTEFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLW 240
Qy 241 RRRRGDAVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPFPGSLEIAQI 300
Db 241 RRRRGDAVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPFPGSLEIAQI 300
Qy 301 SQYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPEPFSQKSLTKDESSRAWT 360
Db 301 SQYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPEPFSQKSLTKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366
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XX PN WO2004056869-A1.
 XX PD 08-JUL-2004.
 XX PF 20-DEC-2003; 2003WO-DK000924.
 XX PR 20-DEC-2002; 2002DK-00001983.
 XX PA (SEVE-) 7TM PHARMA AS.
 XX PI Lange BH, Schwartz TW, Frimurer TM, Rist O;
 XX DR WPI; 2004-525424/50.
 XX DR GENBANK; NP_940799.
 XX PT Novel inverse agonist of ghrelin receptor for medical use such as
 PT treatment or prophylaxis of feeding disorders including overeating e.g.,
 PT bulimia, bulimia nervosa, reduction of body weight, overweight, or
 PT obesity.
 XX PS Example 2; Fig 2; 6ipp; English.
 XX CC The present invention describes an inverse agonist (I) of a ghrelin
 CC receptor for medical use. The ghrelin receptor is a motilin receptor
 CC homologue. Also described: (1) identifying (M1) (I), which involves
 CC contacting a ghrelin receptor with one or more test compounds without the
 CC presence of an agonist for the ghrelin receptor, measuring any change in
 CC the basal activity of the ghrelin receptor, and identifying test
 CC compounds that decreases the basal activity level of the ghrelin receptor
 CC with at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%,
 CC 70%, 75%, 80%, 85%, 90%, 95% or 100%; (2) preparing a pharmaceutical
 CC composition, which involves admixing (I) identified by (M1) with one or
 CC more excipients; and (3) a pharmaceutical composition (II) comprising (I)
 CC together with an excipient. (I) has eating-disorder, anorectic,
 CC analgesic, antianginal, antidiabetic, antilipaeamic and hypotensive
 CC activities, and can be used as a ghrelin receptor inhibitor. (I) is
 CC useful for modulating, by inverse agonism, the activity of a ghrelin
 CC receptor in a mammal. (I) is useful for the preparation of a composition
 CC for modifying the feeding behaviour of a mammal including a human, such
 CC as suppressing hunger or reducing energy intake, or for the treatment or
 CC prophylaxis of feeding disorders including overeating e.g., bulimia,
 CC bulimia nervosa, reduction of body weight, overweight, and/or obesity,
 CC Syndrome X (metabolic syndrome) or any combination of obesity, insulin
 CC resistance, dyslipidaemia, impaired glucose tolerance and hypertension,
 CC Type II diabetes or non insulin dependent diabetes mellitus (NIDDM) or
 CC its complications. The present sequence represents the human ghrelin
 CC receptor amino acid sequence, which is used in the exemplification of the
 CC present invention. The human ghrelin receptor gene is located on
 CC chromosome 3, more specifically to 3q26.31. The human ghrelin receptor is
 CC also known as the growth hormone secretagogue receptor isoform 1a (see
 CC Genbank NP_940799).
 XX SQ Sequence 366 AA;

Query Match
 Best Local Similarity 100.0%; Score 1905; DB 8; Length 366;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWNATPEEPGNLTADLDWDASFGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
 Db 1 MWNATPEEPGNLTADLDWDASFGNDSLGDELLQLFPAPLLAGVTATCVALFVVGAG 60
 Qy 61 NLLTMLVVSREPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
 Db 61 NLLTMLVVSREPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLLCKLFQ 120
 Qy 121 FVSESCYATVLTITLTSVERYPFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGPIFV 180
 Db 121 FVSESCYATVLTITLTSVERYPFAICPLRAKVVVTKGRVKLVFVFWAFAFCSAGPIFV 180
 Qy 181 LVGVEHNGTDPWDTNCRPTFEAVRSGLLTVMVWSSIFFLPVCLTVLYSLIGRKLW 240
 Db 181 LVGVEHNGTDPWDTNCRPTFEAVRSGLLTVMVWSSIFFLPVCLTVLYSLIGRKLW 240

Db 181 LVGVEHNGTDPWDTNCRPTFEAVRSGLLTVMVWSSIFFLPVCLTVLYSLIGRKLW 240
 Qy 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIAQI 300
 Db 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSPFPGSLIAQI 300
 Qy 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFPFQSKLSTLKDESSRAWT 360
 Db 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFPFQSKLSTLKDESSRAWT 360
 Qy 361 ESSINT 366
 Db 361 ESSINT 366
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 AAAY90666
 ID AAAY90666 standard; protein; 366 AA.
 XX AC AAAY90666;
 XX DT 21-AUG-2000 (first entry)
 XX DE Human mutant G protein-coupled receptor GHSR (V262K).
 XX KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;
 KW antagonist; mutant; mutein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO2000022129-A1.
 XX PD 20-APR-2000.
 XX PF 12-OCT-1999; 99WO-US023938.
 XX PR 13-OCT-1998; 98US-00170496.
 XX PA (AREN-) ARENA PHARM INC.
 XX PI Behan DP, Chalmers DT, Liaw CW;
 XX WPI; 2000-329165/28.
 XX N-PSDB; AAA30732.
 XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents.
 XX Example 2; Page 267-268; 341pp; English.
 CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAAY90643-
 CC AAAY90677 and AAAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
 CC and AAA30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence X-
 CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of

CC compounds without the need for endogenous ligands. Sequences AAY90643-
CC AAY90677 and AAY90683-Y90687 the mutant human GPCRs of the invention
XX
SQ Sequence 366 AA;

Query Match 99.7%; Score 1899; DB 3; Length 366;
Best Local Similarity 99.7%; Pred. No. 6.1e-200;
Matches 365; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNATPSEPGNLTADLDWDASPGNDSLGDELLQLPAPLAGVTATCVAFVVGAG 60
DB 1 MNATPSEPGNLTADLDWDASPGNDSLGDELLQLPAPLAGVTATCVAFVVGAG 60

QY 61 NLLTMLVVSFRFELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQ 120
DB 61 NLLTMLVVSFRFELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQ 120

QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180

QY 181 LVGVEHNGTDPWDTNECRPTFEAVRSGLLTVMWVSSIFFPLPVFCLTVLSLGRKLM 240
DB 181 LVGVEHNGTDPWDTNECRPTFEAVRSGLLTVMWVSSIFFPLPVFCLTVLSLGRKLM 240

QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEFGSLEIAQI 300
DB 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEFGSLEIAQI 300

QY 301 SQYCNLVSFVLFSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKLSLTKDESSRAWT 360
DB 301 SQYCNLVSFVLFSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKLSLTKDESSRAWT 360

QY 361 ESSINT 366
DB 361 ESSINT 366

RESULT 14
ADC22729
ID ADC22729 standard; protein; 366 AA.
XX
AC ADC22729;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human G protein-coupled receptor (GPCR) polypeptide #63.
XX
KW Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
KW intracellular-3 region; IC3; receptor.
XX
OS Homo sapiens.
XX
PN US6555339-B1.
XX
PD 29-APR-2003.
XX
PF 13-OCT-1998; 98US-00170496.
XX
PR 14-APR-1997; 97US-00839449.
PR 14-APR-1998; 98US-00060188.
PR 26-JUN-1998; 98US-0090783P.
PR 07-AUG-1998; 98US-0095677P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Liaw CW, Behan DP, Chalmers DT;
XX
DR WPI; 2003-742861/70.
DR N-PSDB; ADC22728.
XX
PT Creating a constitutively active version of an endogenous human G protein
coupled receptor (GPCR) comprises substituting a specific amino acid in

PT the transmembrane-6 region with a different amino acid, and testing for
PT constitutive activity.
XX
PS Example 2; SEQ ID NO 210; 22lpp; English.
XX
CC The invention relates to a method for treating a non-endogenous,
CC constitutively active version of an endogenous human G protein-coupled
CC receptor (GPCR) that has a transmembrane-6 (TM6) region and an
CC intracellular-3 (IC3) region, by substituting a specific amino acid in
CC the TM6 region with a different amino acid, and testing for constitutive
CC activity. The method is useful for creating a constitutively active
CC version of an endogenous human GPCR that comprises a transmembrane 6
CC region and an intracellular loop 3 region. The altered human GPCR
CC polypeptides are useful for screening test compounds for identification
CC of inverse agonists or partial agonists of GPCR polypeptides, which may
CC have therapeutic uses. The altered GPCRs may also be used in vivo or in
CC vitro in biological research. A nucleic acid encoding the altered GPCR
CC may be used to create a transgenic animal expressing the altered GPCR.
CC The method allows screening for compounds that modulate the activity of a
CC human G protein-coupled receptor without the need for provision of a
CC ligand for the receptor. This is particularly useful in allowing
CC screening of compounds against orphan receptors for which no ligand is
CC currently known. This sequence represents a human GPCR polypeptide of the
CC invention.
SQ Sequence 366 AA;

Query Match 99.7%; Score 1899; DB 7; Length 366;
Best Local Similarity 99.7%; Pred. No. 6.1e-200;
Matches 365; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 NLLTMLVVSFRFELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQ 120
DB 61 NLLTMLVVSFRFELRTTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPNWFGDLCKLFQ 120

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DB 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180

QY 181 LVGVEHNGTDPWDTNECRPTFEAVRSGLLTVMWVSSIFFPLPVFCLTVLSLGRKLM 240
DB 181 LVGVEHNGTDPWDTNECRPTFEAVRSGLLTVMWVSSIFFPLPVFCLTVLSLGRKLM 240

QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEFGSLEIAQI 300
DB 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHVGRYLFKSFEFGSLEIAQI 300

QY 301 SQYCNLVSFVLFSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKLSLTKDESSRAWT 360
DB 301 SQYCNLVSFVLFSAAINPILYNIMSKKYRVAVFRLGFEFPFSQKLSLTKDESSRAWT 360

QY 361 ESSINT 366
DB 361 ESSINT 366

RESULT 15
ADH14202
ID ADH14202 standard; protein; 366 AA.
XX
AC ADH14202;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mutated human GHSR.
XX
KW human; non-endogenous; G protein-coupled receptor; GPCR; receptor;
KW mutant; mutein.
XX

Search completed: April 10, 2006, 17:28:40
Job time : 208.354 secs

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OS Synthetic.
OS Homo sapiens.
XX US2003105292-A1.
XX
XX 05-JUN-2003.
XX
XX 20-SEP-2002; 2002US-00251385.
XX
XX 26-JUN-1998; 98US-0090783P.
XX 07-AUG-1998; 98US-0095677P.
XX 13-OCT-1998; 98US-00170496.
XX
XX (LIAW/) LIAW C W.
XX (BEHA/) BEHAN D P.
XX (CHAL/) CHALMERS D T.
XX
XX Liaw CW, Behan DP, Chalmers DT;
XX
XX WPI; 2003-801247/75.
XX N-PSDB; ADH14201.
XX
XX New constitutively active, non-endogenous version of an endogenous human
XX G protein-coupled receptor for the identification of therapeutic
XX compounds, such as agonists.
XX
XX Example 2; SEQ ID NO 210; 227pp; English.
XX
XX The invention relates to a constitutively active, non-endogenous version
XX of an endogenous human G protein-coupled receptor (GPCR). The GPCR is
XX used for screening therapeutic compounds as inverse agonists, agonists or
XX partial agonists. The GPCR can be also be used to elucidate and
XX understand the roles of GPCRs in normal and diseased humans. The GPCR
XX need not be purified and isolated to be used to screen for therapeutic
XX compounds. The utility of the GPCR as a research tool is enhanced because
XX the role of a particular receptor can be understood before the endogenous
XX ligand is identified. The present sequence is used in the exemplification
XX of the present invention.
XX
XX Sequence 366 AA;
XX
Query Match 99.7%; Score 1899; DB 7; Length 366;
Best Local Similarity 99.7%; Pred. No. 6.1e-200;
Matches 365; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNATPSEEPGFNLTADLDWDASPGNDSIGDELLQLFPAPLAGVTATCVLFVVGIAQ 60
Db 1 MNATPSEEPGFNLTADLDWDASPGNDSIGDELLQLFPAPLAGVTATCVLFVVGIAQ 60
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Db 61 NLLTMLVVSFRFRLTNTNLYLSSMAFSDLLIFLCMPDLVRLWQYRPMNFGDLLCKLFQ 120
QY 121 FVSECTYATVLTITALSVERYFAICPPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
Db 121 FVSECTYATVLTITALSVERYFAICPPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
QY 181 LVGVHEHNGTDPMDTNECRPTEFAVRSGLLTVMVWVSSIFFFLPVCLTVLYSLIGRKLW 240
Db 181 LVGVHEHNGTDPMDTNECRPTEFAVRSGLLTVMVWVSSIFFFLPVCLTVLYSLIGRKLW 240
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Db 241 RRRGDVAVGASLRDQNHQTKVRLAVVVFATILCMLPFHVGRYLFKSPFGSLLEIAQI 300
QY 301 SQYCNLVSFVLFYLSAINEPILYNIMSKKYRVAVFRLLGPEPFSQRKSLTKDESSRAWT 360
Db 301 SQYCNLVSFVLFYLSAINEPILYNIMSKKYRVAVFRLLGPEPFSQRKSLTKDESSRAWT 360
QY 361 ESSINT 366
Db 361 ESSINT 366
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GenCore version 5.1.7
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OM protein - protein search, using sw model

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(without alignments)
587.240 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1905	100.0	366	2	US-09-077-675A-13
2	1905	100.0	366	2	US-09-077-674-13
3	1905	100.0	366	2	US-09-170-496D-88
4	1905	100.0	366	2	US-09-743-742B-7
5	1905	100.0	366	2	US-09-762-661A-5
6	1905	100.0	366	2	US-09-364-425B-45
7	1905	100.0	366	2	US-09-743-475-4
8	1899	99.7	366	2	US-09-170-496D-210
9	1874	98.4	361	2	US-09-077-675A-8
10	1874	98.4	361	2	US-09-077-674-8
11	1789	93.9	364	2	US-09-077-675A-16
12	1789	93.9	364	2	US-09-077-674-16
13	1789	93.9	364	2	US-09-762-661A-6
14	1789	93.9	364	2	US-09-743-475-5
15	1788	93.9	364	2	US-09-743-475-3
16	1771	93.0	366	2	US-09-762-661A-7
17	1771	93.0	366	2	US-09-743-475-6
18	1704	89.4	353	2	US-09-077-675A-3
19	1704	89.4	353	2	US-09-077-674-3
20	1596.5	83.8	349	2	US-09-762-661A-2
21	1569	82.4	302	2	US-09-077-675A-7
22	1569	82.4	302	2	US-09-077-674-7
23	1493	78.4	302	2	US-09-077-675A-2
24	1493	78.4	302	2	US-09-077-674-2
25	1418	74.4	271	2	US-09-077-675A-12
26	1418	74.4	271	2	US-09-077-674-12
27	1388	72.9	289	2	US-09-077-675A-10

28 1388 72.9 289 2 US-09-077-674-10 Sequence 10, Appl
29 1258 66.0 289 2 US-09-077-675A-5 Sequence 5, Appl
30 1258 66.0 289 2 US-09-077-674-5 Sequence 5, Appl
31 863.5 45.3 412 2 US-09-743-742B-8 Sequence 8, Appl
32 460 24.1 418 2 US-09-743-742B-5 Sequence 5, Appl
33 454 23.8 418 2 US-09-826-509-535 Sequence 535, App
34 452.5 23.8 403 2 US-09-170-496D-114 Sequence 114, App
35 452.5 23.8 403 2 US-09-743-742B-4 Sequence 4, Appl
36 452.5 23.8 403 2 US-09-743-742B-10 Sequence 10, Appl
37 450.5 23.6 403 2 US-09-170-496D-224 Sequence 224, App
38 446 23.4 415 2 US-09-341-016A-1 Sequence 1, Appl
39 445 23.4 415 2 US-09-545-944-2 Sequence 2, Appl
40 445 23.4 415 2 US-10-215-619-2 Sequence 2, Appl
41 444 23.3 412 2 US-09-949-016-10101 Sequence 10101, A
42 444 23.3 415 2 US-09-875-076-12 Sequence 12, Appl
43 442 23.2 405 2 US-09-743-742B-2 Sequence 2, Appl
44 442 23.2 405 2 US-09-743-742B-11 Sequence 11, Appl
45 420.5 22.1 353 1 US-08-118-270-45 Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-077-675A-13
; Sequence 13, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-675A-13

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Best Local Similarity 100.0%; Pred. No. 1.8e-154;

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Db	61	NLLTMLVVSFRRLRTTNLYLSMASFSDLLIFLCMPDLVRLWQYRPMWFGDLLCKL	FKQ	120	
QY	121	FVSESCYATVLTITALSVERYFAICPLPRAKVVTGKRVKLVITVWAVAFCSAG	PIFV	180	
Db	121	FVSESCYATVLTITALSVERYFAICPLPRAKVVTGKRVKLVITVWAVAFCSAG	PIFV	180	
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Db	181	LVGVEHENGTDPDWTDNECRTEFAVRSGLLTVMVWSSI	IFFFLPVFCLTVLYSLIGRKLW	240	
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RESULT 2

97,21736

US-09-077-674-13
Sequence 13, Application US/09077674
Patent No. 6531314
GENERAL INFORMATION:
APPLICANT: Arena, Joseph P.
APPLICANT: Cully, Doris F.
APPLICANT: Feighner, Scott D.
APPLICANT: Howard, Andrew D.
APPLICANT: Liberator, Paul A.
APPLICANT: Schaeffer, James M.
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,674
FILING DATE: 3-JUN-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19589P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 13:

97,21730

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-674-13

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DB	361	ESSINT	366				

RESULT 3

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US-09-170-496D-88
; Sequence 88, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous,
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-88

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	Query Match	100.0%;	Score 1905;	DB 2;	Length 366;	
	Best Local Similarity	100.0%;	Pred. No. 1.8e-154;			
	Matches 366;	Conservative	0;	Mismatches	0;	Gaps
						0;
Qy	1	MWNAATSEEPGFNNTLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFWVGTAG	60			
Db	1	MWNAATSEEPGFNNTLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCTVALFWVGTAG	60			
Qy	61	NLLTMLVVSFRELRTTTNNLYLSMSAFSDLLIFLCMPDLVRLWOYRPWNNGDLLCKLFQ	120			
Db	61	NLLTMLVVSFRELRTTTNNLYLSMSAFSDLLIFLCMPDLVRLWOYRPWNNGDLLCKLFQ	120			

Qy 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIVAWAFCSAGPIFV 180
Db 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIVAWAFCSAGPIFV 180
Qy 181 LVGVEHNGTDPDWTNECRPTPEFAVRSGLLTVMVWSSIFFLPVFCLTVLYSLIGRKLW 240
Db 181 LVGVEHNGTDPDWTNECRPTPEFAVRSGLLTVMVWSSIFFLPVFCLTVLYSLIGRKLW 240
Qy 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFVAFILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Db 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFVAFILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Qy 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPFPSQKSLTLKDESSRAWT 360
Db 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPFPSQKSLTLKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366

RESULT 4
US-09-743-742B-7
; Sequence 7, Application US/09743742B
; Patent No. 6599718
; GENERAL INFORMATION:
; APPLICANT: Liu, Qingyun
; APPLICANT: Howard, Andrew D.
; APPLICANT: McKee, Karen Kulju
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RELATED
; TITLE OF INVENTION: RECEPTORS AND NUCLEIC ACIDS
; FILE REFERENCE: 20217P
; CURRENT APPLICATION NUMBER: US/09/743,742B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: PCT/US99/15941
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: 60/092,623
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-743-742B-7

Query Match 100.0%; Score 1905; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.8e-154;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIG 60
Db 1 MNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIG 60
Qy 61 NLTMLVSVRFRELRTTNLYLSSMAFSDLLIFLCMPDLVRLVQYRPNFNGDLLCKLFQ 120
Db 61 NLTMLVSVRFRELRTTNLYLSSMAFSDLLIFLCMPDLVRLVQYRPNFNGDLLCKLFQ 120
Qy 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIVAWAFCSAGPIFV 180
Db 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIVAWAFCSAGPIFV 180
Qy 181 LVGVEHNGTDPDWTNECRPTPEFAVRSGLLTVMVWSSIFFLPVFCLTVLYSLIGRKLW 240
Db 181 LVGVEHNGTDPDWTNECRPTPEFAVRSGLLTVMVWSSIFFLPVFCLTVLYSLIGRKLW 240
Qy 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFVAFILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Db 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFVAFILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Qy 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPFPSQKSLTLKDESSRAWT 360
Db 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPFPSQKSLTLKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366

RESULT 6
US-09-364-425B-45
; Sequence 45, Application US/09364425B
; Patent No. 6653086
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.

Db 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPFPSQKSLTLKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366

RESULT 5
US-09-762-661A-5
; Sequence 5, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-762-661A-5

Query Match 100.0%; Score 1905; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.8e-154;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIG 60
Db 1 MNATPSEEPGFNLTLADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIG 60
Qy 61 NLTMLVSVRFRELRTTNLYLSSMAFSDLLIFLCMPDLVRLVQYRPNFNGDLLCKLFQ 120
Db 61 NLTMLVSVRFRELRTTNLYLSSMAFSDLLIFLCMPDLVRLVQYRPNFNGDLLCKLFQ 120
Qy 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIVAWAFCSAGPIFV 180
Db 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVTKGRVKLVIFVIVAWAFCSAGPIFV 180
Qy 181 LVGVEHNGTDPDWTNECRPTPEFAVRSGLLTVMVWSSIFFLPVFCLTVLYSLIGRKLW 240
Db 181 LVGVEHNGTDPDWTNECRPTPEFAVRSGLLTVMVWSSIFFLPVFCLTVLYSLIGRKLW 240
Qy 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFVAFILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Db 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFVAFILCWLPHFVGRYLFKSPFPGSLEIAQI 300
Qy 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPFPSQKSLTLKDESSRAWT 360
Db 301 SOYCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGPFPSQKSLTLKDESSRAWT 360
Qy 361 ESSINT 366
Db 361 ESSINT 366

RESULT 6
US-09-364-425B-45
; Sequence 45, Application US/09364425B
; Patent No. 6653086
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.

	/	PRIOR APPLICATION NUMBER:	PCT/US99/15375	
	/	PRIOR FILING DATE:	1999-07-08	
	/	PRIOR APPLICATION NUMBER:	60/092,361	
	/	PRIOR FILING DATE:	1998-07-10	
	/	NUMBER OF SEQ ID NOS:	10	
	/	SOFTWARE:	PastSeq for Windows Version 4.0	
	/	SEQ ID NO 4		
	/	LENGTH:	366	
	/	TYPE:	PRT	
	/	ORGANISM:	Homo sapiens	
	/	US-09-743-475-4		
		Query Match	100.0%; Score 1905; DB 2; Length 366;	
		Best Local Similarity	100.0%; Pred. No. 1.8e-154;	
		Matches	366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy		1	MNNATPSEPGFNLTADLDWDASPCGNDSLGDDELLQLFPAPLIAGVTATCVALFVVGIAG 60 	
Dd		1	MNNATPSEPGFNLTADLDWDASPCGNDSLGDDELLQLFPAPLIAGVTATCVALFVVGIAG 60 	
Qy		61	NLLTMLVSRFRRLTNTNLYLSSMAFSDLLIFLCMPLDLVRWLQRWPNWFGLDCKLFQ 120 	
Dd		61	NLLTMLVSRFRRLTNTNLYLSSMAFSDLLIFLCMPLDLVRWLQRWPNWFGLDCKLFQ 120 	
Qy		121	FVSSECTYATVLITITALSVERYFAICPIIRAKVVWTGRVKLVIVFIWA VAFCSAGPIFV 180 	
Dd		121	FVSSECTYATVLITITALSVERYFAICPIIRAKVVWTGRVKLVIVFIWA VAFCSAGPIFV 180 	
Qy		181	LGVGEHENGTDPDWNTECHPTPEAVRSGLLTVMWVSSIFFFLPVCLTLVLYSLIGRKLW 240 	
Dd		181	LGVGEHENGTDPDWNTECHPTPEAVRSGLLTVMWVSSIFFFLPVCLTLVLYSLIGRKLW 240 	
Qy		241	RRRRGDAVVGSARDQNQHQTVMKLA AVVFPAFILCMLPHVGRYLFSKSPEPSGLEIAOI 300 	
Dd		241	RRRRGDAVVGSARDQNQHQTVMKLA AVVFPAFILCMLPHVGRYLFSKSPEPSGLEIAOI 300 	
Qy		301	SQVCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFEPPSQRKSTLKDESRAWT 360 	
Dd		301	SQVCNLVSVFLFYLSAAINPILYNIMSKKYRVAVFRLLGFEPPSQRKSTLKDESRAWT 360 	
Qy		361	ESSINT 366 	
Dd		361	ESSINT 366 	
		RESULT 8		
		US-09-170-496D-210		
		/ Sequence 210, Application US/09170496D		
		/ Patent No. 6555339		
		GENERAL INFORMATION:		
		/ APPLICANT: Behan, Dominic P.		
		/ APPLICANT: Chalmers, Derek T.		
		/ APPLICANT: Liaw, Chen W.		
		/ TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G		
		/ TITLE OF INVENTION: Receptors		
		/ FILE REFERENCE: AREN-0040		
		/ CURRENT APPLICATION NUMBER: US/09/170,496D		
		/ CURRENT FILING DATE: 1998-10-13		
		/ NUMBER OF SEQ ID NOS: 294		
		/ SOFTWARE: Patentin version 3.1		
		/ SEQ ID NO 210		
		/ LENGTH: 366		
		/ TYPE: PRT		
		/ ORGANISM: Homo sapiens		
		US-09-170-496D-210		
		Query Match	99.7%; Score 1899; DB 2; Length 366;	
		Best Local Similarity	99.7%; Pred. No. 5.8e-154;	
		Matches	365; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy		1	MNNATPSEPGFNLTADLDWDASPCGNDSLGDDELLQLFPAPLIAGVTATCVALFVVGIAG 60 	
Dd		1	MNNATPSEPGFNLTADLDWDASPCGNDSLGDDELLQLFPAPLIAGVTATCVALFVVGIAG 60 	

QY 61 NLLTMLVVRPRELTTNNLYLSSMAFSDLLIFLCMPDLVLRLWQYRPNFEDLLCKLFQ 120
DB 61 NLLTMLVVRPRELTTNNLYLSSMAFSDLLIFLCMPDLVLRLWQYRPNFEDLLCKLFQ 120
QY 121 FVSECTATVLTITALSVERFEAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
DB 121 FVSECTATVLTITALSVERFEAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
QY 181 LVGEHENGTPDWTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLW 240
DB 181 LVGEHENGTPDWTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLW 240
QY 241 RRRGDAVVGASLRDQNHKQTKMLAVVVFAPILCWLPHFVGRYLFKSPFPGSLIAQI 300
DB 241 RRRGDAVVGASLRDQNHKQTKMLAVVVFAPILCWLPHFVGRYLFKSPFPGSLIAQI 300
QY 301 SOYCNLYSVFLYLSAANPILYNIMSKYRVAVFRLGPFPSQKSLTKDSSRAWT 360
DB 301 SOYCNLYSVFLYLSAANPILYNIMSKYRVAVFRLGPFPSQKSLTKDSSRAWT 360
QY 361 ESSINT 366
DB 361 ESSINT 366

RESULT 9
US-09-077-675A-8
; Sequence 8, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-675A-8

Query Match 98.4%; Score 1874; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.7e-152;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 PSEPGFNLTADLDWDASPGNDSIGDELLQLFPAPLLAGVTATCVALFVVGIAGNLLTM 65
DB 1 PSEPGFNLTADLDWDASPGNDSIGDELLQLFPAPLLAGVTATCVALFVVGIAGNLLTM 60
QY 66 LVSRFRELRTTNNLYLSSMAFSDLLIFLCMPDLVLRLWQYRPNFEDLLCKLFQFVSES 125
DB 61 LVSRFRELRTTNNLYLSSMAFSDLLIFLCMPDLVLRLWQYRPNFEDLLCKLFQFVSES 120
QY 126 CTYATVLTITALSVERFEAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFVVGVE 185
DB 121 CTYATVLTITALSVERFEAICFPLRAKVVTKGRVKLVIFVIWAVAFCSAGPIFVVGVE 180
QY 186 HENGTPDWTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLWRRRG 245
DB 181 HENGTPDWTNECRPTFAVRSGLLTVMWVSSIFFFLPVFCLTVLYSLIGRKLWRRRG 240
QY 246 DAVVGASLRDQNHKQTKMLAVVVFAPILCWLPHFVGRYLFKSPFPGSLIAQISOYCN 305
DB 241 DAVVGASLRDQNHKQTKMLAVVVFAPILCWLPHFVGRYLFKSPFPGSLIAQISOYCN 300
QY 306 LVSPVLFYLSAANPILYNIMSKYRVAVFRLGPFPSQKSLTKDSSRAWTESSIN 365
DB 301 LVSPVLFYLSAANPILYNIMSKYRVAVFRLGPFPSQKSLTKDSSRAWTESSIN 360
QY 366 T 366
DB 361 T 361
RESULT 10
US-09-077-674-8
; Sequence 8, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,674
; FILING DATE: 3-JUN-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19589P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/077,674
FILING DATE: 3-JUN-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 195899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-077-674-16

Query Match 93.9%; Score 1789; DB 2; Length 364;
Best Local Similarity 95.6%; Pred. No. 1.4e-144;
Matches 350; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Qy	1	MNATPSEEPGFNLTLADLDWDASPGNDSLGLDQLLPAPLAGVATATCVALFVVGIG	60
Db	1	MNATPSEEPGFNLTLADLDWDASPGNDSLGLDQLLPAPLAGVATATCVALFVVGIG	59
Qy	61	LLTMLVVSFRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLVQYRPNFNGDLLCKLFQ	120
Db	60	LLTMLVVSFRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLVQYRPNFNGDLLCKLFQ	119
Qy	121	FVSESCYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFIWAVAFCSAGPIFV	180
Db	120	FVSESCYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFIWAVAFCSAGPIFV	179
Qy	181	LVGVEHNGTDPDWTNCRPTFAVRSGLLTMVWVSSIFPFLPVFCLTVLYSLIGRKLW	240
Db	180	LVGVEHNGTDPDWTNCRPTFAVRSGLLTMVWVSSIFPFLPVFCLTVLYSLIGRKLW	239
Qy	241	RRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPGSLAIAQI	300
Db	240	-RRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPGSLAIAQI	298
Qy	301	SOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLLGPEPFSQRKSLTKDESSRAWT	360
Db	299	SOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLLGPEPFSQRKSLTKDESSRAWT	358
Qy	361	ESSINT 366	
Db	359	KSSINT 364	

RESULT 13

US-09-762-661A-6
Sequence 6, Application US/09762661A
Patent No. 6645726
GENERAL INFORMATION:
APPLICANT: Howard, Andrew D.
APPLICANT: Palyha, Oksana C.
APPLICANT: Smith, Roy G.
APPLICANT: Tan, Carina P.
TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
RECEPTOR

FILE REFERENCE: 20207P
CURRENT APPLICATION NUMBER: US/09/762,661A
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US99/17915
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 60/095,960
PRIOR FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 364
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-762-661A-6

Query Match 93.9%; Score 1789; DB 2; Length 364;
Best Local Similarity 95.6%; Pred. No. 1.4e-144;
Matches 350; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Qy	1	MNATPSEEPGFNLTLADLDWDASPGNDSLGLDQLLPAPLAGVATATCVALFVVGIG	60
Db	1	MNATPSEEPGFNLTLADLDWDASPGNDSLGLDQLLPAPLAGVATATCVALFVVGIG	59
Qy	61	LLTMLVVSFRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLVQYRPNFNGDLLCKLFQ	120
Db	60	LLTMLVVSFRPRELRTTNLYLSSMAFSDLLIFLCMPDLVRLVQYRPNFNGDLLCKLFQ	119
Qy	121	FVSESCYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFIWAVAFCSAGPIFV	180
Db	120	FVSESCYATVLTITALSVERYFAICPLRAKVVVTKGRVKLVFIWAVAFCSAGPIFV	179
Qy	181	LVGVEHNGTDPDWTNCRPTFAVRSGLLTMVWVSSIFPFLPVFCLTVLYSLIGRKLW	240
Db	180	LVGVEHNGTDPDWTNCRPTFAVRSGLLTMVWVSSIFPFLPVFCLTVLYSLIGRKLW	239
Qy	241	RRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPGSLAIAQI	300
Db	240	-RRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPFHVGRYLFKSPGSLAIAQI	298
Qy	301	SOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLLGPEPFSQRKSLTKDESSRAWT	360
Db	299	SOYCNLVSVFLFYLSAAINPILYNIMSKYRVAVFRLLGPEPFSQRKSLTKDESSRAWT	358
Qy	361	ESSINT 366	
Db	359	KSSINT 364	

RESULT 14

US-09-743-475-5
Sequence 5, Application US/09743475
Patent No. 6682908
GENERAL INFORMATION:
APPLICANT: Smith, Roy G.
APPLICANT: Van der Ploeg, Leonardus H. T.
APPLICANT: Howard, Andrew D.
APPLICANT: Zheng, Hui
APPLICANT: McKee, Karen Kulju
APPLICANT: Jiang, Michael M.
TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
RECEPTOR
FILE REFERENCE: 20218P
CURRENT APPLICATION NUMBER: US/09/743,475
CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: PCT/US99/15375
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/092,361
PRIOR FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 364
TYPE: PRT

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; ORGANISM: Rattus norvegicus
US-09-743-475-5

Query Match      93.9%; Score 1789; DB 2; Length 364;
Best Local Similarity 95.6%; Pred. No. 1.4e-144;
Matches 350; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

QY 1 MNATPSEPGNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIGAG 60
DB 1 MNATPSEPEPNVTL-DLDWDASPGNDSLDPELLPLPAPLLAGVTATCVAFVVGISG 59

QY 61 NLLTMLVVSRRFRELRTTNLYLSSNAFSDLLIFLCMPDLDLVRLWQYRPNWFGDLLCKLFQ 120
DB 60 NLLTMLVVSRRFRELRTTNLYLSSNAFSDLLIFLCMPDLDLVRLWQYRPNWFGDLLCKLFQ 119

QY 121 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVIFVIWAVAFCSAGPIFV 180
DB 120 FVSECTYATVLTITALSVERYFAICFPLRAKVVVTKGRVKLVILVIVAVAFCSAGPIFV 179

QY 181 LVGVEHENGTDPDWTDNECRPTPEFAVRSGLLTVMWVSSIFPFLPVFCITVLYSLIGRKLW 240
DB 180 LVGVEHENGTDPRDTNECRATEFAVRSGLLTVMWVSSVFFFLPVFCITVLYSLIGRKLW 239

QY 241 RRRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHFVGRYLFKSFPFGSLEIAQI 300
DB 240 -RRRGDAVVGASLRDQNHKQTVKMLAVVVFAPILCWLPHFVGRYLFKSFPFGSLEIAQI 298

QY 301 SOYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLLGFPFPFSQORKLSTLKDESSRAWT 360
DB 299 SOYCNLVSFVLFYLSAAINPILYNIMSKKYRVAVFRLLGFPFSQORKLSTLKDESSRAWT 358

QY 361 ESSINT 366
DB 359 KSSINT 364

Search completed: April 10, 2006, 17:35:43
Job time : 52.528 secs
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RESULT 15
US-09-743-475-3
; Sequence 3, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-743-475-3

Query Match      93.9%; Score 1788; DB 2; Length 364;
Best Local Similarity 95.4%; Pred. No. 1.7e-144;
Matches 349; Conservative 6; Mismatches 9; Indels 2; Gaps 2;

QY 1 MNATPSEPGNLTADLDWDASPGNDSLGDELLQLFPAPLLAGVTATCVAFVVGIGAG 60
DB 1 MNATPSEPEPNVTL-DLDWDASPGNDSLDPELLPLPAPLLAGVTATCVAFVVGISG 59

QY 61 NLLTMLVVSRRFRELRTTNLYLSSNAFSDLLIFLCMPDLDLVRLWQYRPNWFGDLLCKLFQ 120
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